

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 11:35:53 ; Search time 962.98 seconds
(without alignments)
1471.172 Million cell updates/sec

Title: US-08-700-737-11

Perfect score: 396
Sequence: 1 ATGAGTTGCTGTAGCT.....GACCAAGCTGGAATPAAA 396

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database :

GenEmbl.*
1: gb_bal.*
2: gb_bal.*
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4: gb_in.*
5: gb_ov.*
6: gb_ov.*
7: gb_ph.*
8: gb_ph.*
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10: gb_pl2.*
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42: gb_pl2.*
43: gb_pl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Score Match Length DB ID Description

1	375.2	94.7	396	13	MMU16688	U16688 Mus musculus
2	356.2	89.9	396	13	MUSIGKBN	M15814 Mouse Ig ac
3	331.2	83.6	339	13	MUSIGKCOL	M24275 Mouse Ig ge
4	323.2	81.6	805	13	MUSIGKIDAH	L12156 W3129; Mus
5	320	80.8	336	13	MUSIGK2AK	X74588 M. musculus
6	319.8	80.8	323	13	MUSIGKAPD	M64152 Mus musculus
7	319.8	80.8	323	13	MUSIGKAFM	M64161 Mus musculus
8	318.4	80.4	387	13	HS001812	AJ001812 Mus muscu
9	318.4	80.4	339	13	MUSIGKCOI	M24272 Mouse Ig ge
10	318.4	80.4	339	13	MUSIGKCOK	M24274 Mouse Ig ge
11	318.2	80.4	351	13	MMU22904	U22904 Mus musculu
12	305.2	77.7	404	13	RATIGCD2L	M87786 Rat (hybrid
13	303.8	76.1	442	13	MMBV1613L	X53642 M.musculus
14	301.2	76.1	538	13	MMIGVK	X00045 Mouse mRNA
15	300.6	75.9	538	13	MUSIGKAT	R00709 Mouse Ig ka
16	298.4	75.4	417	13	MMU62051	U62051 Mus musculu
17	298	75.3	333	13	MMU01885	U01885 Mus musculu
18	297.6	75.2	342	13	AF003287	AF003287 Mus muscu
19	293.6	74.1	394	6	AR022585	AR022585 Sequence
20	293.6	74.1	393	13	AF045491	AF045491 Mus muscu
21	293.6	74.1	436	13	MMU012556	AJ012556 Mus muscu
22	293.6	74.1	416	13	MUSIGKCLL	M20828 Mouse IgG2a
23	293.6	74.1	426	13	MUSIGVK	M55313 Mouse Igk p
24	293.6	74.1	394	13	S67233	S67233 Igg3Vl-muc1
25	293.6	74.1	456	13	MMU39901	U39901 Mus musculu
26	290.4	73.3	393	13	AF013576	AF013576 Mus muscu
27	290.4	73.3	393	13	MUSIGK324A	M32382 Mus musculu
28	288.8	72.9	393	13	MUSIGK514	L39088 Mus musculu
29	288.8	72.9	393	13	MUSIGK940A	L39104 Mus musculu
30	288.8	72.9	393	13	MUSIGK1240	M32384 Mus musculu
31	287.2	72.5	394	6	AR022571	AR022571 Sequence
32	287.2	72.5	393	13	AF045490	AF045490 Mus muscu
33	287.2	72.5	393	13	MUSIGK13A	L39105 Mus musculu
34	286	72.2	384	6	AR013851	AR013851 Sequence
35	285.6	72.1	393	13	AF045494	AF045494 Mus muscu
36	285.6	72.1	393	13	MUSIGK4420	L39087 Mus musculu
37	285.6	72.1	393	13	MUSIGK1025	M32381 Mus musculu
38	285.6	72.1	432	13	MMU62054	U62054 Mus musculu
39	285.6	72.1	956	13	MMKAPLI	X87231 M.musculus
40	284	71.7	427	6	A25561	A25561 H.sapiens B
41	284	71.7	434	6	A25576	A25576 M.musculus
42	284	71.7	434	6	I26965	I26965 Sequence 4
43	284	71.7	427	6	I26967	I26967 Sequence 8
44	284	71.7	420	13	MMU841LEV	X65775 M.musculus
45	282.4	71.3	394	6	AR022601	AR022601 Sequence

ALIGNMENTS

RESULT 1
LOCUS MMU16688 396 bp mRNA ROD 06-FEB-1997
DEFINITION Mus musculus Ig light chain leader and variable region VK II gene
ACCESSION U16688
KEYWORDS family mRNA, partial cds.
NID g1041798
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 396)
AUTHORS White,K.D., Frank,M.B., Foundling,S. and Waxman,F.J.
TITLE Effect of Immunoglobulin variable region structure on C3b and C4b deposition
JOURNAL Mol. Immunol. 33 (9), 759-768 (1996)
MEDLINE 96406984
REFERENCE 2 (bases 1 to 396)
AUTHORS Frank,B.
TITLE Direct Submission
JOURNAL Submitted (27-OCT-1994) Bart Frank, Arthritis and Immunology

KEYWORDS	NID	9197085	C-region; J-region; germ-line; immunoglobulin light chain; immunoglobulin-kappa variable region; processed gene.
ORGANISM <td>Mus musculus</td> <td>(clone 36.1.2D) mRNA.</td> <td></td>	Mus musculus	(clone 36.1.2D) mRNA.	
REFERENCE <td>Murine; Mus.</td> <td>1 (bases 1 to 339)</td> <td></td>	Murine; Mus.	1 (bases 1 to 339)	
AUTHORS <td>Matsuda, T. and Kabat, E. A.</td> <td></td> <td></td>	Matsuda, T. and Kabat, E. A.		
TITLE <td>Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1-6) dextran</td> <td></td> <td></td>	Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1-6) dextran		
JOURNAL <td>J. Immunol.</td> <td>142 (3), 863-870 (1989)</td> <td></td>	J. Immunol.	142 (3), 863-870 (1989)	
MEDLINE <td>89110062</td> <td></td> <td></td>	89110062		
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<td>FGGGTKLEIKR"</td> <td></td> <td></td>	FGGGTKLEIKR"		
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ORIGIN			
Query Match	83.6%	Score 331.2;	DB 13; Length 339;
Best Local Similarity	99.1%;	Pred. No. 1.1e-97;	
Matches 333;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
OY	61	GATGTGTTGGGACCAACCTCCACTCCCGCTGCAGCTTTGGAGATCAAGTTCT	120
DB	1	GATGTGTTGGGACCAACCTCCACTCCCGCTGCAGCTTTGGAGATCAAGTTCT	60
OY	121	ATCTCTTCAGGTCAGTACAGATCTTCCAAAGATTATGGACACCTATTGCTTGG	180
DB	61	ATCTCTTCAGGTCAGTACAGATCTTCCAAAGATTATGGACACCTATTGCTTGG	120
OY	181	TACCTGCACAAAGCCTGGCCAGTCTCCACAGCTCTCATCTATGGGATTTCCACAGATT	240
DB	121	TACCTGCACAAAGCCTGGCCAGTCTCCACAGCTCTCATCTATGGGATTTCCACAGATT	180
OY	241	TCTGGGGTCCAGACAGATTCAAGTTCAGTGGCAGTGGTTAGGGACAGATTTCACACTCAAGTC	300
DB	181	TCTGGGGTCCAGACAGATTCAAGTTCAGTGGCAGTGGTTAGGGACAGATTTCACACTCAAGTC	240
OY	301	AGCACAATAAAGCCTGAGAGACTTGGGANTGTTTACTGCTTACAGATGACATCAGCGC	360
DB	241	AGCACAATAAAGCCTGAGAGACTTGGGANTGTTTACTGCTTACAGATGACATCAGCGC	300
OY	361	TACAGCTTCGAGAGGGGACCAAGCTGGAATAAATA	396
DB	301	TACAGCTTCGAGAGGGGACCAAGCTGGAATAAATA	336
RESULT 4			
MUSIGRIDAH	805 bp	DNA	ROD 18-JUL-1994
LOCUS	W3129;	Mus musculus Igk (W3129) chain gene with insertion/deletion mutations.	
DEFINITION			
ACCESSION	L12156		
NID	9197336		
KEYWORDS	Immunoglobulin kappa-chain; immunoglobulin light chain.		
SOURCE	Mus musculus (strain BALB/c) DNA.		
ORGANISM	Mus musculus		
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.		

	REFERENCE	1 (bases 1 to 805)
AUTHORS	Chou,C.L. and Morrison,S.L.	
TITLE	Intron sequences determine the expression of kappa light chain genes	
JOURNAL	Mol. Immunol. 31 (2), 99-107 (1994)	
MEDLINE	94142762	
REFERENCE	2 (bases 1 to 805)	
AUTHORS	Chou,C.L. and Morrison,S.L.	
TITLE	A common sequence motif near nonhomologous recombination breakpoints involving Ig sequences	
JOURNAL	J. Immunol. 150 (12), 5350-5360 (1993)	
MEDLINE	93294290	
REFERENCE	3 (bases 1 to 805)	
AUTHORS	Chou,C.L. and Morrison,S.L.	
TITLE	An insertion-deletion event in murine immunoglobulin kappa gene resembles mutations at heavy-chain disease loci	
JOURNAL	Somat. Cell Mol. Genet. 19 (2), 131-139 (1993)	
MEDLINE	93289445	
FEATURES	Location/Qualifiers	
source	1..805	
	/organism="Mus musculus"	
	/sub_species="domesticus"	
	/db_xref="taxon:10090"	
	/tissue_type="myeloma"	
sig_peptide	join(1..49,456..466)	
	/gene="Igk"	
	/label=leader	
gene	1..466	
	/gene="Igk"	
	48..55	
	/gene="Igk"	
	/note="putative splice donor sequence"	
intron	50..455	
	/gene="Igk"	
	145..146	
	/gene="Igk"	
misc_feature	/note="cryptic splice acceptor site in cell line 5S"	
	/citation=[1]	
	152..153	
misc_feature	/gene="Igk"	
	/note="deletion breakpoint site in cell line 5S"	
	/citation=[1]	
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misc_feature	/gene="Igk"	
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	294..313	
misc_feature	/gene="Igk"	
	/note="deleted in cell line R15"	
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misc_signal	/gene="Igk"	
	/note="putative splice acceptor sequence"	
	467..805	
exon	/gene="immunoglobulin kappa variable region"	
	/label=V-kappa	
gene	467..805	
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	537..538	
misc_feature	/gene="immunoglobulin kappa variable region"	
	/note="cryptic splice acceptor site, used in cell lines R15, 5S"	
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	628..781	
	/citation=[2]	
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ORIGIN		

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	/db_xref="PID:g1333980"	
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	70..117	
misc_feature	/gene="IGLV75"	
	/note="CDR I region IGLV75"	
misc_feature	118..162	
	/gene="IGLV75"	
	/note="FRM II region IGLV75"	
misc_feature	163..183	
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	/note="CDR II region IGLV75"	
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	/gene="IGLV75"	
	/note="FRM III region IGLV 75"	
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	/note="CDR III region IGLV75"	
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Query Match	80.8%; Score 320; DB 13; Length 336;	
Best Local Similarity	97.0%; Pred. No. 4; 9e-94;	
Matches 326; Conservative 0; Mismatches 10; Indels 0; Gaps 0;		
QY	61 GATGTTGTGTGACTCAAACTCACTCTCCCTGCTGCTGACCTTTGGAGATCAAGTTTCT 120	
Db	1 GATGTTGTGTGACTCAAACTCACTCTCCCTGCTGCTGACCTTTGGAGATCAAGTTTCT 60	
QY	121 ATCTCTTGACAGGTCTAGTCAGAGTCTTTGCAAAAGTTATGGGAACACTTATTGTCTTGG 180	
Db	61 ATCTCTTGACAGGTCTAGTCAGAGTCTTTGCAAAAGTTATGGGAACACTTATTGTCTTGG 120	
QY	181 TACTGCAACAAGCCTGGGCACTGCCACAGCTCCTCATCTATGGGATTGCCAAGAGATT 240	
Db	121 TACTGCAACAAGCCTGGGCACTGCCACAGCTCCTCATCTATGGGATTGCCAAGAGATT 180	
QY	241 TCTGGGGGTCAGACAGAGTTCACTGTCAGTGGTTCAGAGGAGAGATTTCACACTCAAGATC 300	
Db	181 TCTGGGGGTCAGACAGAGTTCACTGTCAGTGGTTCAGAGGAGAGATTTCACACTCAAGATC 240	
QY	301 AGCACAAATTAAGCCTGAGAGCTTGGGAATGTATTACTGCTTACAAAGGTACACATCAGCCG 360	
Db	241 AGCACAAATTAAGCCTGAGAGCTTGGGAATGTATTACTGCTTACAAAGGTACACATCAGCCG 300	
QY	361 TACACGTTCCGAGGGGGGACCAAGCTGGAATAAATAA 396	
Db	301 TACACGTTCCGAGGGGGGACCAAGCTGGAATAAATAA 336	
RESULT 6		
MUSICKAFD		
LOCUS	MUSICKAFD 323 bp mRNA ROD 13-JUN-1996	
DEFINITION	Mus musculus Ig active kappa-chain mRNA V-region.	
ACCESSION	M64152	
NID	g196688	
KEYWORDS	V-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 323) Caton,A.J., Stark,S.E., Kavalier,J., Staudt,L.M., Schwartz,D. and	

TITLE Gerhard W.
Many variable region genes are utilized in the antibody response of
JOURNAL BALB/c mice to the influenza virus A/PR/8/34 hemagglutinin
MEDLINE J. Immunol. 147 (5), 1675-1686 (1991)
COMMENT Specific for influenza virus A/PR/8/34 hemagglutinin.
FEATURES Location/Qualifiers
Source
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/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
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CDS
BASE COUNT 78 a 79 c 79 g 87 t
ORIGIN
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Best Local Similarity 99.4%; Pred. No. 5.7e-94;
Matches 321; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 61 GATGTTGGTGACACCAACTCCACTCTCCCTGCTGACGTTGGAGATCAAGTTCT 120
DB 1 GATGTTGGTGACACCAACTCCACTCTCCCTGCTGACGTTGGAGATCAAGTTCT 60
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DB 61 ATCTCTGACAGGTCTAGTCAGAGTCTTGCAAGAGTTATGGAAACCACTATTGTCTGG 120
QY 181 TACCTGCACAAGCTGGCCAGTCTCCACAGCTCTCATCTATGGATTTCCAAAGATT 240
DB 121 TACCTGCACAAGCTGGCCAGTCTCCACAGCTCTCATCTATGGATTTCCAAAGATT 180
QY 241 TCTGGGGTCCAGACAGGTTCAAGTGGCTTCAAGGACAGATTTCACACTCAAGATC 300
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QY 301 AGCAATTAAGGCTGAGGACTTGGGAATGATTAAGTCTTCAAGTTCACATAGCCG 360
DB 241 AGCAATTAAGGCTGAGGACTTGGGAATGATTAAGTCTTCAAGTTCACATAGCCG 300
QY 361 TACAGTTCCGAGGGGGGACCAA 383
DB 301 TACAGTTCCGAGGGGGGACCAA 323
RESULT 7
MUSIGRAF 323 bp mRNA ROD 13-JUN-1996
LOCUS Mus musculus Ig active kappa-chain mRNA V-region.
DEFINITION M64161
ACCESSION 9196706
NID V-region; immunoglobulin light chain; immunoglobulin-kappa;
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euthera;
REFERENCE Murine; Mus.
AUTHORS Murine; A.J., Stark, S.E., Kavalier, J., Staudt, L.M., Schwartz, D. and
TITLE Many variable region genes are utilized in the antibody response of
JOURNAL BALB/c mice to the influenza virus A/PR/8/34 hemagglutinin
J. Immunol. 147 (5), 1675-1686 (1991)

MEDLINE 91349593
COMMENT Specific for influenza virus A/PR/8/34 hemagglutinin.
FEATURES Location/Qualifiers
Source
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PGOSPQLIYGISNRFSGVDRFSGSSGIDFTLKISTIKPEDIGMYCLOGTHQPYT
FGGCT"
CDS
BASE COUNT 78 a 79 c 79 g 87 t
ORIGIN
Query Match 80.8%; Score 319.8; DB 13; Length 323;
Best Local Similarity 99.4%; Pred. No. 5.7e-94;
Matches 321; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 61 GATGTTGGTGACACCAACTCCACTCTCCCTGCTGACGTTGGAGATCAAGTTCT 120
DB 1 GATGTTGGTGACACCAACTCCACTCTCCCTGCTGACGTTGGAGATCAAGTTCT 60
QY 121 ATCTCTGACAGGTCTAGTCAGAGTCTTGCAAGAGTTATGGAAACCACTATTGTCTGG 180
DB 61 ATCTCTGACAGGTCTAGTCAGAGTCTTGCAAGAGTTATGGAAACCACTATTGTCTGG 120
QY 181 TACCTGCACAAGCTGGCCAGTCTCCACAGCTCTCATCTATGGATTTCCAAAGATT 240
DB 121 TACCTGCACAAGCTGGCCAGTCTCCACAGCTCTCATCTATGGATTTCCAAAGATT 180
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DB 241 TCTGGGGTCCAGACAGGTTCAAGTGGCTTCAAGGACAGATTTCACACTCAAGATC 240
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DB 241 AGCAATTAAGGCTGAGGACTTGGGAATGATTAAGTCTTCAAGTTCACATAGCCG 300
QY 361 TACAGTTCCGAGGGGGGACCAA 383
DB 301 TACAGTTCCGAGGGGGGACCAA 323
RESULT 8
HS001812 387 bp mRNA ROD 30-MAR-1998
LOCUS Mus musculus partial mRNA sequence for immunoglobulin light chain
DEFINITION V-region (clone 2C7/K18F).
ACCESSION A001812
NID 93004453
KEYWORDS immunoglobulin; variable region.
SOURCE house mouse.
MUSIGRAF 387 bp mRNA ROD 30-MAR-1998
LOCUS Mus musculus
DEFINITION Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Euthera;
REFERENCE Rodentia; Sciurognathi; Muridae; Murine; Mus.
AUTHORS McElveen, J., Clark, M.R., Smith, S.J., Sewell, H.F. and Shakhb, F.
TITLE Primary sequence and molecular model of the variable region of a
mouse monoclonal anti-der P I antibody showing the same epitope
specificity as human IGE: Production of a mouse monoclonal
anti-idiotypic that recognises a cross-reactive idiotypic on human
IgE
REFERENCE Unpublished
AUTHORS Clark, M.R.
TITLE Direct Submission

JOURNAL Submitted (27-SEP-1997) Clark M.R., Pathology Department,
University of Cambridge, Tennis Court Road, Cambridge, CB2 1QP, UK.
FEATURES Location/Qualifiers
source 1. 387
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BASE COUNT 96 a 100 c 91 g 100 t
ORIGIN

Query Match 80.4%; Score 318.4; DB 13; Length 387;
Best Local Similarity 96.7%; Pred. No. 1.7e-93;
Matches 325; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 61 GATGTTGTGAGTCAAACTCCACTCCCTGCTGTCAGCTTTGGAGATCAAGTTCT 120
|||||
DB 1 GATGTTGTGAGTCAAACTCCACTCCCTGCTGTCAGCTTTGGAGATCAAGTTCT 60
QY 121 ATCTCTGAGGCTCTAGTCAAGTCTTGAAGATTAAGGAACCTATTGTCTTG 180
|||||
DB 61 ATCTCTGAGGCTCTAGTCAAGTCTTGAAGATTAAGGAACCTATTGTCTTG 120
QY 181 TACCTGCACAGCCTGGCAGTCTCCACAGCTCTCATATGGAATTCACAGATT 240
|||||
DB 121 TACCTGCACAGCCTGGCAGTCTCCACAGCTCTCATATGGAATTCACAGATT 180
QY 241 TCTGGGGTCCAGACAGTTCAGTGCAGTGTTCAGGACATTTTCACTCAAGATC 300
|||||
DB 181 TCTGGGGTCCAGACAGTTCAGTGCAGTGTTCAGGACATTTTCACTCAAGATC 240
QY 301 AGCACAATAAAGCCTGAGGAGCTTGGGAATATTACTGCTTACAGGTACATCAGCCG 360
|||||
DB 241 AGCACAATAAAGCCTGAGGAGCTTGGGAATATTACTGCTTACAGGTACATCAGCCG 300
QY 361 TACAGCTTCGGAGGGGGACCAAGCTGGAAATATAA 396
|||||
DB 301 TGGACGTTGCGTGGAGGACCAAGCTGGAAATATAA 336

RESULT 9
MUSIGKCOI 339 bp mRNA ROD 07-MAR-1995
LOCUS Mouse Ig germline X24 kappa-chain mRNA (V-J1), partial cds.
DEFINITION M24772
ACCESSION
KEYWORDS
C-region; J-region; germline; immunoglobulin light chain;
immunoglobulin-kappa variable region; processed gene.
SOURCE
Mus musculus (clone 16.4.12p) mRNA.
ORGANISM
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognath; Myomorpha; Muridae;
Murinae; Mus.
1 (bases 1 to 339)
REFERENCE
AUTHORS Matsuda,T. and Kabat,E.A.
TITLE Variable region cDNA sequences and antigen binding specificity of
mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled
to proteins. T-dependent analogues of alpha(1---6)dextran
J. Immunol. 142 (3), 863-870 (1989)

MEDLINE 89110062
FEATURES Location/Qualifiers
source 1. 339
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="16.4.12p"
<1..>339
/note="Ig kappa-chain (V-J1)"
/codon_start=1
/db_xref="pid:g197080"
/translation="DVLMTQTPLESLPVSEFGDQVSISSRSSGLANSYNTLYSLYHLK
PQSPQLITIGISIDRSFSGVDPDRFSGSGSDFTLKISTIKPEDLMYICLOGTHQPMW
FGGTRLEIKRADAAPTVSIFFPSSSQ"

BASE COUNT 86 a 81 c 84 g 88 t
ORIGIN

Query Match 80.4%; Score 318.4; DB 13; Length 339;
Best Local Similarity 96.7%; Pred. No. 1.6e-93;
Matches 325; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 61 GATGTTGTGAGTCAAACTCCACTCCCTGCTGTCAGCTTTGGAGATCAAGTTCT 120
|||||
DB 1 GATGTTGTGAGTCAAACTCCACTCCCTGCTGTCAGCTTTGGAGATCAAGTTCT 60
QY 121 ATCTCTGAGGCTCTAGTCAAGTCTTGAAGATTAAGGAACCTATTGTCTTG 180
|||||
DB 61 ATCTCTGAGGCTCTAGTCAAGTCTTGAAGATTAAGGAACCTATTGTCTTG 120
QY 181 TACCTGCACAGCCTGGCAGTCTCCACAGCTCTCATATGGAATTCACAGATT 240
|||||
DB 121 TACCTGCACAGCCTGGCAGTCTCCACAGCTCTCATATGGAATTCACAGATT 180
QY 241 TCTGGGGTCCAGACAGTTCAGTGCAGTGTTCAGGACATTTTCACTCAAGATC 300
|||||
DB 181 TCTGGGGTCCAGACAGTTCAGTGCAGTGTTCAGGACATTTTCACTCAAGATC 240
QY 301 AGCACAATAAAGCCTGAGGAGCTTGGGAATATTACTGCTTACAGGTACATCAGCCG 360
|||||
DB 241 AGCACAATAAAGCCTGAGGAGCTTGGGAATATTACTGCTTACAGGTACATCAGCCG 300
QY 361 TACAGCTTCGGAGGGGGACCAAGCTGGAAATATAA 396
|||||
DB 301 TGGACGTTGCGTGGAGGACCAAGCTGGAAATATAA 336

RESULT 10
MUSIGKCOI 339 bp mRNA ROD 07-MAR-1995
LOCUS Mouse Ig germline J558 kappa-chain mRNA (V-J4), partial cds.
DEFINITION M24274
ACCESSION
KEYWORDS
C-region; J-region; germline; immunoglobulin light chain;
immunoglobulin-kappa variable region; processed gene.
SOURCE
Mus musculus (clone 35.8.2H) mRNA.
ORGANISM
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognath; Myomorpha; Muridae;
Murinae; Mus.
1 (bases 1 to 339)
REFERENCE
AUTHORS Matsuda,T. and Kabat,E.A.
TITLE Variable region cDNA sequences and antigen binding specificity of
mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled
to proteins. T-dependent analogues of alpha(1---6)dextran
J. Immunol. 142 (3), 863-870 (1989)

JOURNAL MEDLINE 89110062
FEATURES Location/Qualifiers
source 1. 339
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="35.8.2H"
<1..>339
/note="Ig kappa-chain (V-J4)"

Db 381 CACACTTTGGCCAGGGAGCACAAGCTGGAGATCAA 416

[illegible]

FEATURES
 Contact: Wilson RK
 Masht-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LINT; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28m1 rev2 ET from Amer sham.
 Location/Qualifiers

```

source
1. .363
/organism="Homo sapiens"
/ote="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligod(T) primer (5'
TGTTCACATCTGTGAGTGGAGCGCCGCGTCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="609678"
/clone_1lb="Soares ovary tumor NBH07"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1. >363
/db_xref="GDB:6039712"

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Query Match	52.4%	Score 207.6	DB 20	Length 363
Best Local Similarity	74.6%	Pred. No. 12e-55		
Matches 261	Conservative	0	Mismatches 89	Indels 0
				Gaps 0

[illegible][illegible]

RESULT	4
H27034	
LOCUS	
DEFINITION	H27034 467 bp mRNA EST 12-JUL-1995
ACCESSION	U165005.r1 Homo sapiens cDNA clone 163113 5' similar to gb:X72467
NID	IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);.
KEYWORDS	H27034
SOURCE	9897024
	EST.
	human clone=163113 library=Soares Breast 3NBHst vector=pT7T3D
	(Pharmacia) with a modified polylinker host=DH10B (ampicillin

ORGANISM
Homo sapiens
Eukaryote; Metazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
and M.Fatima Bonalato.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 467)
Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman J., Hulman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rife K., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston R., Williamson A., Wohlmann P. and
Wilson R.
The WashU-Merck EST Project
Unpublished (1995)

CONTACT: Wilson RK
 Washu-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel.: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 352
 Source: IMAGE Consortium, LNTL
 This clone is available royalty-free through LNTL ; contact the
 IMAGE Consortium (info@image.lntl.gov) for further information.
 Location/Qualifiers
 1..467

[illegible]

ORGANISM	Homosapiens
Eukaryotae: Chordata: Vertebrata: Mammalia: Eutheria:	
Primates: Catarrhini: Hominoidea: Homo.	
REFERENCE	1 (bases 1 to 335)
AUTHORS	Hillier, L., Allen, M., Bowles, L., Dubouche, T., Gelsel, G., Jost, S., Kitzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., "

RESULT	10
AA496610	
LOCUS	287 bp
DEFINITION	mrna EST 12-AUG-1997
	z338d06.r1 Soares ovary tumor NBH07 Homo sapiens CDNA clone 755962
	5' similar to gb:872467 IG KAPPA CHAIN PRECURSOR V-II REGION


```

High quality sequence stops: 1
Source: IMAGE Consortium, LINTL
This clone is available royalty-free through LINTL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality.
location/Qualifiers
1
257

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BASE COUNT	53 a	67 c	62 g	63 t	12 others
ORIGIN					

Query Match	36.68;	Score 144.8;	DB 10;	Length 257;
Best Local Similarity	71.48;	Pred. No. 8,4e-36;		
Matches 182;	Conservative 0;	Mismatches 73;	Indels 0;	Gaps 0;

[illegible]

Search completed: May 11, 1999, 11:44:10
Job time: 497 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 11:37:53 ; Search time 88.51 Seconds
(without alignments)
841.712 Million cell updates/sec

Title: US-08-700-737-11

Sequence: 1 ATGAAGTTGCCCTGTTAGGCT.....GGACCAAGCTGGAATAAAA 396

Scoring table:

Searched: 240622 seqs, 94065609 residues

Database : N_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	396	100.0	356	1	V20077	DNA encoding murJin
2	396	100.0	535	1	V20086	Consensus DNA sequ
3	359.2	90.7	413	1	V20075	DNA encoding the I
4	296.8	74.9	717	1	T62934	Murine anti-porcine
5	296.8	74.9	5300	1	T62938	3F4 human IgG4 exp
6	293.6	74.1	394	1	062763	Murine KC-4 immunc
7	293.6	74.1	394	1	062788	Murine KC-4 immunc
8	292	73.7	394	1	087531	VL sequence of ant
9	288.8	72.9	394	1	062803	Humanised murine K
10	288.8	72.9	394	1	087533	Humanised anti-KC
11	287.2	72.5	394	1	062749	Murine BRE-3 immu
12	287.2	72.5	394	1	062774	Murine BRE-3 immu
13	286	72.2	384	1	V56383	Murine ICR-8.1 V-R
14	286	72.2	384	1	V56387	Murine antibody IC
15	285.6	72.1	537	1	014651	R6-5-D6 anti-ICAM
16	284	71.7	437	1	034529	Chimeric Mab ligh
17	284	71.7	427	1	036536	BR55-2 light chain
18	284	71.7	447	1	T31332	Anti-Idiotypic monoc
19	284	71.7	424	1	T98835	Coding sequence f
20	282.4	71.3	434	1	Q36534	BR55-2 murine IgG
21	282.4	71.3	394	1	062790	Humanised murine E
22	282.4	71.3	717	1	T88870	Humanised murine E
23	282.4	71.3	396	1	V37265	L chain subunit of
24	282.4	71.3	717	1	V67336	CDNA encoding a va
25	279.2	70.5	8897	1	V18692	Anti-human Fas mon
26	277.6	70.1	537	1	014601	Plasmid pTWD-CVTK
27	276	69.7	422	1	V22075	Encodes murine ant
28	274.4	69.3	420	1	V60831	DNA encoding the I
29	272.8	68.9	432	1	008606	Variable light cha
30	272.8	68.9	432	1	T43439	Co-1 Light Chain V
31	269.4	68.0	459	1	Q11292	MAB Co-1 murine ch
32	269.2	68.0	330	1	Q43746	Encodes murine mo
33	266.8	67.4	861	1	081500	Sequence encoding
34	266.8	67.4	861	1	T45347	sFv anti-rv sequen
35	266.4	67.3	388	1	V66574	Single chain sFv a
36	255	64.4	782	1	086755	Anti-Fas Mab Ch11
37	252	63.6	413	1	Q20071	Anti-dansyl single
38	251.2	63.4	336	1	Q97505	MK16-L chain. Chi
39	250.4	63.2	876	1	V10390	Light chain variab
40	250.4	63.2	8897	1	V18693	Monoclonal antibod
41	249.6	63.0	336	1	T36587	Plasmid pDI60J1.L
42	248.8	62.8	747	1	Q21098	DNA encoding murin
43	248.8	62.8	723	1	V10375	psceFNQ11 encodin
						Anti-CD40 monoclon

QY 241 TCTGGGTCACAGAGCTTACAGTGGTTCAGGACAGATTTCACACTCAGATC 300
 DB 241 TCTGGGTCACAGAGCTTACAGTGGTTCAGGACAGATTTCACACTCAGATC 300
 QY 301 AGCACAATAAAGCCTGAGAGCTTGGGAATGTATTACTGCTTACAGATACATCAGCCG 360
 DB 301 AGCACAATAAAGCCTGAGAGCTTGGGAATGTATTACTGCTTACAGATACATCAGCCG 360
 QY 361 TACAGCTTGGAGGGGGGACCAAGCTGGAATATAA 396
 DB 361 TACAGCTTGGAGGGGGGACCAAGCTGGAATATAA 396

RESULT 2

V20086
 ID V20086 standard; DNA; 535 BP.
 AC V20086;
 DT 14-JUL-1998 (first entry)
 DE Consensus DNA sequence of the murine variable light chain region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease; ss.
 OS Mus sp.
 FT Key Location/Qualifiers
 FT CDS 16..435
 FT sig_peptide /tag= a
 FT 16..75 /note= "no stop codon given"
 FT mat_peptide /tag= b
 FT 76..435
 FT /tag= c
 PN WO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J.
 DR WPI: 98-159172/14.
 DR P-PSDB; W53817.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PS asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 3: 145pp: English.
 CC The present sequence represents the consensus nucleotide sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse light chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal adressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in mucosal
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20083-84. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis
 CC Sequence 535 BP; 126 A; 128 C; 132 G; 149 T;

Query Match

100.0%; Score 396; DB 1; Length 535;

Best Local Similarity 100.0%; Pred. No. 4, 2e-116;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTTGCCCTGTAGGCTGTGGTCTCTGTGCTGAGATTCCTGTTCCGAGGT 60
 |||

DB 16 ATGAAGTTGCCCTGTAGGCTGTGGTCTCTGTGCTGAGATTCCTGTTCCGAGGT 75
 QY 61 GATGTGTGGTACCAAACTCCACTCCCTGGCTGTACAGTTGGAGATCAAGTTCT 120
 DB 76 GATGTGTGGTACCAAACTCCACTCCCTGGCTGTACAGTTGGAGATCAAGTTCT 135
 QY 121 ATCTCTGAGAGCTTACAGAGCTTCCAAAGATTATGGACACCTATTGTCTGG 180
 DB 136 ATCTCTGAGAGCTTACAGAGCTTCCAAAGATTATGGACACCTATTGTCTGG 195
 QY 181 TACCTGCACACAGCTGGCCAGCTTCCACAGCTCCCTCATCTATGGATTTCACAGATT 240
 DB 196 TACCTGCACACAGCTGGCCAGCTTCCACAGCTCCCTCATCTATGGATTTCACAGATT 255
 QY 241 TCTGGGTCACAGAGCTTACAGTGGTTCAGGACAGATTTCACACTCAGATC 300
 DB 256 TCTGGGTCACAGAGCTTACAGTGGTTCAGGACAGATTTCACACTCAGATC 315
 QY 301 AGCACAATAAAGCCTGAGAGCTTGGGAATGTATTACTGCTTACAGATACATCAGCCG 360
 DB 316 AGCACAATAAAGCCTGAGAGCTTGGGAATGTATTACTGCTTACAGATACATCAGCCG 375
 QY 361 TACAGCTTGGAGGGGGGACCAAGCTGGAATATAA 396
 DB 376 TACAGCTTGGAGGGGGGACCAAGCTGGAATATAA 411

RESULT 3

V20075
 ID V20075 standard; DNA; 413 BP.
 AC V20075;
 DT 14-JUL-1998 (first entry)
 DE DNA encoding the light chain of a humanised murine Act-1 antibody.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease; ss.
 OS Synthetic.
 OS Mus sp.
 FT Key Location/Qualifiers
 FT CDS 1..413
 FT sig_peptide /tag= a
 FT 1..60 /transl_except= (pos: 412..413, aa: Pro)
 FT 61..413 /note= "no stop codon given"
 FT mat_peptide /tag= b
 FT 61..413
 FT /tag= c
 PN WO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J.
 DR WPI: 98-159172/14.
 DR P-PSDB; W53812.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PS asthma, graft versus host disease and sarcoidosis
 PS Claim 17; Fig 12: 145pp: English.
 CC The present sequence encodes the light chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MadCAM-1, which is present of high endothelial
 CC venules in mucosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can

	Intron	3350.	.4080	/ *tag-	j
FT					
FT					

FT	1.000
FT	4081. .4233
exon	

KW inflammation; disorder; T cell activation; macrophage; Crohn's disease;
 KW adult respiratory distress syndrome; stroke; multiple sclerosis; asthma;
 KW rheumatoid arthritis; tumour growth; human immune deficiency virus;
 KW infection; diabetes; graft vs host disease; passive immunisation; ss.
 OS Mus sp.
 PD US5773218-A.
 PD 30-JUN-1998.
 PE 07-JUN-1995. 482882.
 PR 05-AUG-1994; US-286754.
 PR 27-JAN-1992; US-827689.
 PR 26-MAY-1992; US-889724.
 PR 05-JUN-1992; US-894061.
 PR 22-JAN-1993; US-009266.
 PR 26-JAN-1993; WO-000787.
 PR 05-AUG-1993; US-102852.
 PR 07-JUN-1995; US-482882.
 PA (ICOS-) ICOS CORP.
 PI Gallatin MM, Vazeux R;
 DR WPI, 98-386989/33.
 DR P-PSDB: W76124.
 PT Identifying compounds that modulate interaction of intercellular
 PT adhesion molecule R - with ligands HSI-beta and tubulin using
 PT two-hybrid assay, useful for treating inflammation, T cell
 PT activation etc.
 PS Example 13; Column 111-112; 108PP; English.
 CC This sequence is a murine ICR-8.1 V-K region amplified PCR product. This
 CC sequence is used in the isolation of a novel human intercellular adhesion
 CC molecule, ICAM-R. This sequence is used in a method which investigates
 CC modulators of the interaction between ICAM-R and the 14.3.3 family member
 CC HSI-beta and tubulin. An anti-ICAM-R antibody optionally coupled to toxin
 CC or radionuclide, or an ICAM-R peptide, can block, inhibit or stimulate
 CC ligand/receptor interactions involving ICAM-R, particularly its effector
 CC functions involved in (non)specific immune responses. ICAM-R related
 CC agents may be used to treat or monitor inflammation, disorders involving
 CC T cell activation or macrophages, e.g. adult respiratory distress
 CC syndrome, stroke, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis, asthma, tumour growth, human immune deficiency virus
 CC infection, diabetes, graft vs. host disease and many others. Antibodies
 CC may also be used for passive immunisation, for purifying, detecting or
 CC quantifying ICAM-R and for identifying ICAM-R expressing cells.
 QO Sequence 384 BP; 92 A; 96 C; 97 G; 98 T;

Query Match	Similarity	Score	DB 1:	Length
Best Local	84.8%	Pred. No. 2.2e-81:		
Matches 319:	Conservative	1:	Mismatches 56:	Indels 0; Gaps 0
QY	21	GTTCGCTCTTCGTTGTTCTGATTCGATTCCTTTTCCGGAGGTGATGTGTGTCACCTCAAC	80	
Db	9	GCTGTGGTGGATCGATGATGTTGTGATTCCTTTTCCAGTATGACGCGTGTATGACCCAAAC	68	
QY	81	TCACACTTCCTCGCTGTGACGCTTTGGAGATCAAGTTTCTATCTCTTGGAGGCTTAATGA	140	
Db	69	TCCACTTCCTCCGCTGTCACGCTTGGAGATCAAGCTTCATCTTTGACATCTAGTA	128	
QY	141	GAGTTTGCAGAGATTTATGGGAACACCATTTGTTCTGTGTACCTGCACAAAGCTTGGCCA	200	
Db	129	GAGCTTTGTACACCAATTAATGGAGAACCATTTTACATTGTGTACCTGCACAAAGCCAGGCCA	188	
QY	201	GTCTCCACAGCCCTCACTATATGGGATTTCCAAAGATTTCTGGGGTCCAGACAGGTT	260	
Db	189	GTCTCCACAGCTCCCTGATCTTACAAAGTTTCCAAAGATTTCTGGGGTCCAGACAGGTT	248	
QY	261	CAGTGGCAGTGGTTAGGGAGACAGATTTACACTCAAGATCAGACACAAATAAAGCTTGAGGA	320	
Db	249	CAGTGGCAGTGGATCAGGGAGACAGATTTTACACTCAAGCTCAGACAGAGTGGAGGCTTGAGGA	308	
QY	321	CTTGGGAATGTATTAATCTCTTCAAGAGTACACATCAAGCCGTACAGTTTGGAGGGGGGAC	380	
Db	309	TCTGGAGTTATTTCTCTCTCTCAAGATACACATGTCTGACAGTTTGGAGGGGGGAC	368	
QY	381	CAAGCTGGAAATAAAA	396	

Db 369 CAAGCTGGAATAA 384

RESULT 14

ID V54857 standard; DNA; 384 BP.
V54857;
AC V54857;
DT 18-NOV-1998 (first entry)
DE Murine antibody ICR-8.1 light chain DNA.
KW Human; ICAM-R; intercellular adhesion molecule; adhesion; treatment;
KW inflammatory condition; asthma; tumour growth; metastasis;
KW viral infection; antibody ICR-8.1; ss.
OS Mus sp.
PN US5811517-A.
PD 22-SEP-1998.
PF 07-JUN-1995; 483389.
PR 05-AUG-1994; US-286754.
PR 27-JAN-1992; US-827689.
PR 26-MAY-1992; US-889724.
PR 05-JUN-1992; US-894061.
PR 02-DEC-1993; US-009266.
PR 05-AUG-1993; US-102852.
PR 07-JUN-1995; US-483389.
PA (ICOS-) ICOS CORP.
PI Gallatin MM, Vazeux R;
DR WPI: 98-530940/45.
DR P-PSDB; W71254.
PT DNA encoding mutant ICAM-R poly:peptide(s) - useful for diagnosis
PT and treatment of cell adhesion based disease conditions e.g.
PT inflammation or asthma
PS Example 13; Columns 109-110; 11pp; English.
CC The present sequence encodes the light chain of murine antibody
CC ICR-8.1. This antibody is specific for ICAM-R (intercellular adhesion
CC molecule-R). ICAMs are polypeptides that are expressed on blood vessel
CC endothelial cell surfaces and are involved in the adhesion events in
CC various conditions. ICAM-R variants (see W71264-69) can be used to
CC treat or monitor inflammatory conditions involving specific or
CC non-specific immune responses, asthma, tumour growth and/or metastasis
CC and viral infections. The ICAM variants are produced recombinantly, from
CC expression libraries of mutated sequences, and the ones that are
CC claimed are the ones that have been found to be especially involved in
CC adhesion events. They can also be used to raise antibodies, also for
CC use as therapeutic or diagnostic agents.
SQ Sequence 384 BP; 92 A; 96 C; 97 G; 98 T;

	Query Match	Best Local Similarity	Matches	Conservative	72.2%	Score 286;	DB 1;	Length 384;
		84.8%;			1;	Mismatches 56;	Indels	0;
								Gaps 0;
QY	21	GTGGTGGCTTCTGTGTGTCTGATTCGATTCCTGGTTCGCGAGGTGATGTGTGGTACTCAAC	80					
Db	9	GCTGTGGTGGTGAATGATCTGGATTCCTGTTCCAGTGTAGACGGTGTGATGATCCCAAC	68					
QY	81	TCCACTCTCCCTGCCGTGCAGCTTTGGAGATCAAGATTCTATCTCTTCAGGTCTATGCA	140					
Db	69	TCCACTCTCCCTGCCGTGCAGCTTTGGAGATCAAGCCTCCATCTCTTCAGATCTATGCA	128					
QY	141	GAGCTTCCAAAGATTGTGGAAACACCTATTGTCTGGTACCTGCACAGCCCTGGCA	200					
Db	129	GAGCTTGTACAGATATGAGACACCTATTTCATTGTGACCTGCAGAAGCCAGGCCA	188					
QY	201	GTCTCACAGCTCCTCATCTATGGATTTCACACAGATTTCTGGGGGTCCACAGAGGTT	260					
Db	189	GTCTCCACAGCTCCTGATCTCAAAAGTTTCCACCGATTTTCTGGGGTCCACAGAGGTT	248					
QY	261	CAGTGGCAGTGGTTCAGGGACAGATTTCACACTCAAGATCAGACAAATAAAGCCTGAGGA	320					
Db	249	CAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGCTCAGACAGATGGAGGCTGAGGA	308					
QY	321	CTTGGGAATGATTAATCTCTTCAAAAGTACATACGCCGTACACAGTTCCGAGGGGGGAC	380					
Db	309	TCCTGGAGTTATTTATTTCTCTCTCAAAAGTACATATGTTCCGTACACAGTTCCGAGGGGGGAC	368					

QY 381 CAAGCTGGAAATATAA 396
 Db 369 CAAGCTGGAAATATAA 384

RESULT 15

Q14651

ID Q14651 standard; cDNA; 537 BP.

AC Q14651;

DT 14-FEB-1992 (first entry)

DE R6-5-D6 anti-ICAM-1 light chain.

KM Intercellular adhesion molecule-1; antibody; chimeric; ds.

OS Mus musculus.

FH Key Location/Qualifiers

FT signal_peptide 19..75

FT /*tag- a

FT 19..537

FT /*tag- b

PN WO9116928-A.

PD 14-NOV-1991.

PE 29-APR-1991; U02946.

PR 27-APR-1990; GB-009548.

PA (CELL-) CELTECH LTD.

PI (BOEH) BOEHRINGER INGELHEIM PHA.

PI Adair JR, Robinson MK, Bright SM, Rothlein RA;

DR WPI; 91-353534/48.

DR P-PSDB; R15199.

PT New humanised chimeric anti-ICAM-1 antibodies - useful in

PT treating inflammation e.g. psoriasis and ulcerative colitis to

PT suppress metastasis of haematopoietic tumour cell and in

PT diagnosis.

PS Claim 10; Fig 1; 85pp; English.

CC The sequence comprises the 5' untranslated region, signal sequence,

CC variable region and part of the constant region for the R6-5-D6

CC murine MAb light chain. The hybridoma cell line R6-5-D6 producing

CC the anti ICAM-1 Ab was provided by Boehringer Ingelheim

CC Pharmaceuticals Inc. The cells were grown and mRNA isolated and

CC used to prepare cDNA for a library in pSP64 vector DNA. The

CC library was grown in E. coli HB101 and colonies screened using a

CC probe complementary to a sequence in the mouse kappa constant

CC region or with a 980 bp BamHI-EcoRI restriction fragment of a

CC previously isolated mouse IgG2a constant region clone. Six

CC positive clones were isolated and rescreened. Positive clones from

CC the second round of screening were grown and the DNA inserts

CC sequenced. The DNA was used to construct humanised Abs having

CC chimeric variable regions, esp. with IgG human constant region

CC domains. The Abs can be used to treat inflammation, to suppress

CC metastasis of haematopoietic tumour cells and growth of ICAM-1

CC expressing tumour cells, to treat viral infection, to suppress

CC extravascular migration of virally infected leucocytes and to treat

CC asthma.

CC See also Q14652 and Q14830.

SQ Sequence 537 BP; 135 A; 134 C; 128 G; 139 T;

Query Match

Best Local Similarity 72.1%; Score 285.6; DB 1; Length 537;

Matches 334; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 ATGAAGTGGCTGTAGGCTGTGGTCTCTGTGATTCCTGTTCCGGAGGT 60

Db 19 ATGAAGTGGCTGTAGGCTGTGGTCTCTGTGATTCCTGATTCAGAGT 75

QY 61 GATGTTGTGTGACTCAAACTCACCTCCCTGCTGAGCTTTGAGATCAAGTTCT 120

Db 76 GATGTTGTGTGACTCAAACTCACCTCCCTGCTGAGCTTTGAGATCAAGCTCC 135

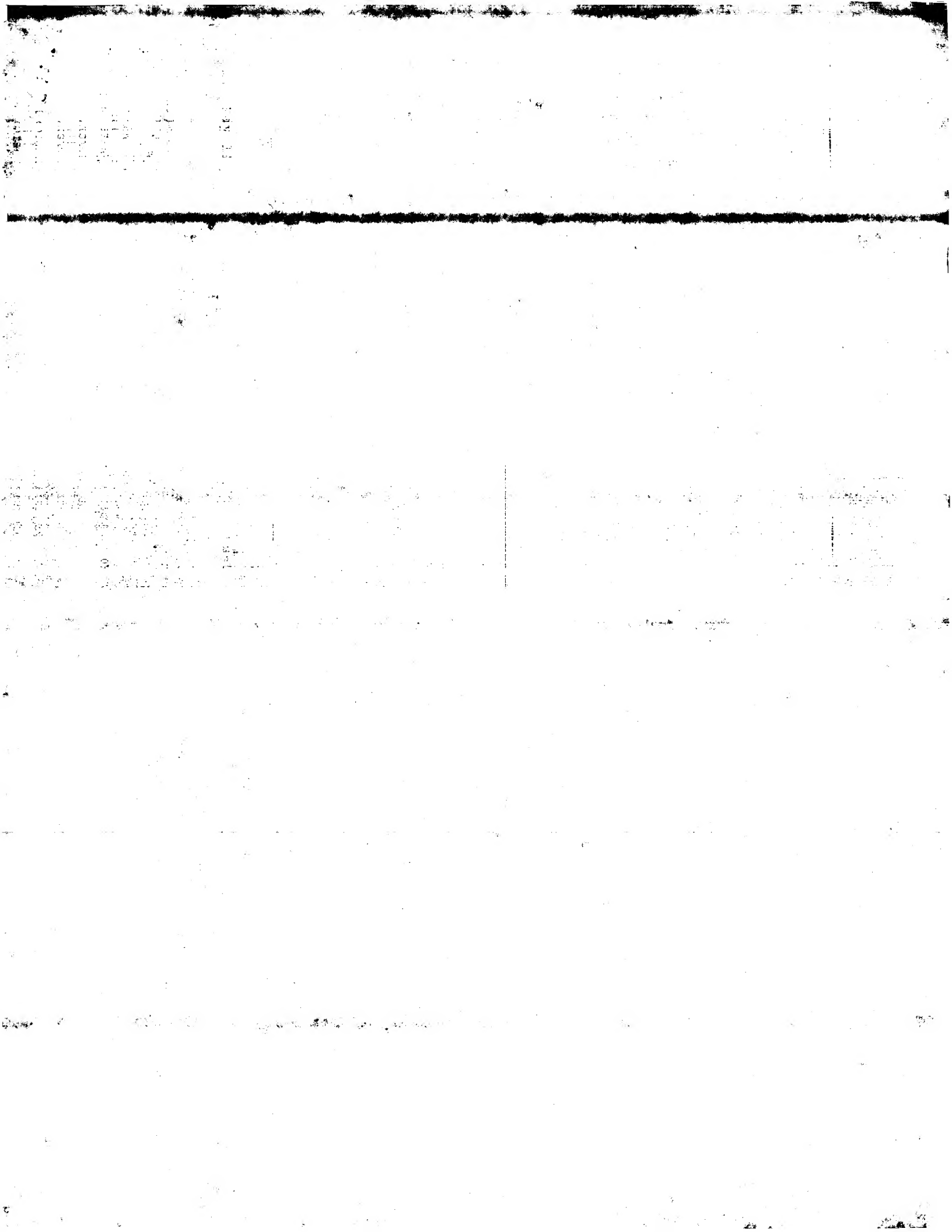
QY 121 ATCTCTTGCAAGTCTAGTCAAGTCTTGAAGAAGTATGGAACACCTATTGCTGG 180

Db 136 ATCTCTTGCAAGTCTAGTCAAGTCTTGAAGAAGTATGGAACACCTATTGCTGG 195

QY 181 TACCTGCACAAAGCTGGCCAGTCTCCACAGCTCCTCATCTATGGGATTTCCAAAGATT 240

Db 196 TACCTGCACAAAGCTGGCCAGTCTCCACAGCTCCTCATCTATGGAATTTCCAAAGATT 255
 QY 241 TCTGGGGTCCAGACAGAGTTCAGTGTGAGGACAGATTTCCACACTCAAGATC 300
 Db 256 TCTGGGGTCCAGACAGAGTTCAGTGTGAGGACAGATTTCCACACTCAAGATC 315
 QY 301 AGCACAATAAAGCTGAGAGCTTGGGAATGTATTACTGCTTACAAAGTACATCAGCG 360
 Db 316 AGCAGAGTGGAGGCTGAGATCTGGAGTTTATTCGCTCAAGATGACATGTTCT 375
 QY 361 TACAGCTGGAGGGGGGACCAAGCTGGAATATAA 396
 Db 376 CTCAGCTGGAGGGGGGACCAAGCTGGAATATAA 411

Search completed: May 11, 1999, 12:03:26
 Job time: 1533 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:18:27 ; Search time 30.48 Seconds
(without alignments)
162.230 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695
Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLOGTHQPTFGGCTKLEIK 132

Scoring table: BLOSUM62

Searched: 116738 seqs, 37460341 residues

Database: PIR-58.*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	620	89.2	132	2	B25912	Ig kappa chain pre
2	576	82.6	113	2	E30560	Ig kappa chain V r
3	574	82.6	113	2	E30560	Ig kappa chain V r
4	563	81.0	112	2	S37203	Ig kappa chain V r
5	560.5	80.6	131	2	B39276	Ig light chain pre
6	553.5	79.6	131	2	B34904	Ig kappa chain pre
7	549.5	79.1	131	2	C34904	Ig kappa chain pre
8	548.5	78.9	114	2	PL0202	anti-DNA autoantib
9	546.5	78.6	131	2	B32513	Ig kappa chain pre
10	545.5	78.5	131	2	B30577	Ig kappa chain pre
11	540.5	77.8	132	3	D34904	Ig kappa chain pre
12	540.5	77.8	132	3	PH0106	anti-digoxin trans
13	539	77.6	131	2	D29380	Ig kappa chain pre
14	537.5	77.3	131	2	G34903	Ig kappa chain pre
15	537.5	77.3	111	2	PS0074	Ig kappa chain V r
16	536.5	77.2	131	2	S09259	Ig kappa chain pre
17	529.5	76.2	131	2	S52449	Ig kappa chain V r
18	523.5	75.3	131	2	PC0178	Ig kappa chain pre
19	521	75.0	130	2	E29380	Ig kappa chain pre
20	502	72.2	133	2	S23230	Ig kappa chain pre
21	497.5	71.6	119	2	A49032	Ig kappa chain V r
22	496	71.4	142	2	S22902	Ig kappa chain V r
23	493.5	71.0	118	2	S24503	Ig kappa chain V r
24	493	70.9	133	2	S42611	HNNVK protein prec
25	492.5	70.9	113	2	S24536	Ig kappa chain V r
26	491	70.6	133	1	K2HURP	Ig kappa chain pre
27	490.5	70.6	118	2	S24533	Ig kappa chain V r
28	489	70.4	112	2	E27887	Ig kappa chain V r
29	488.5	70.3	118	2	S24500	Ig kappa chain V r
30	488	70.2	118	2	PT0359	Ig kappa chain V r
31	488	70.2	112	2	A31807	Ig kappa chain V r
32	487.5	70.1	116	2	S24529	Ig kappa chain V r
33	487.5	70.1	118	2	S24535	Ig kappa chain V r
34	486	69.9	112	2	A49715	Ig kappa chain V r
35	486	69.9	219	2	S16112	Ig kappa chain V r
36	484	69.6	110	2	S26335	Ig kappa chain V r
37	484	69.6	121	2	S67944	Ig kappa chain pre
38	483	69.5	112	2	S32189	Ig kappa chain V r
39	483	69.5	113	2	PL0203	anti-DNA autoantib

40	481.5	69.3	140	2	S22658	Ig kappa chain pre
41	481.5	69.3	118	2	S24532	Ig kappa chain V r
42	481	69.2	112	2	B31485	Ig kappa chain V r
43	481	69.2	219	2	PC4203	Ig kappa chain (mo
44	480.5	69.1	118	2	S24530	Ig kappa chain V r
45	480	69.1	112	2	D27887	Ig kappa chain V r

ALIGNMENTS

RESULT 1
B25912
Ig kappa chain precursor V region (W3129) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Mar-1998
C:Accession: B25912
R:Borden, P.; Kabat, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443, 1987
A:Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and light
A:Reference number: A94147; MUID:87175689
A:Accession: B25912
A:Molecule type: mRNA
A:Residues: 1-132 <BOR>
A:Cross-References: GB:M15874; NID:g196839; PID:g196840
A:Note: the authors translated the codon CTC for residue 120 as Ser
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence (fragment) #status predicted <Sig>
F:20-132/Product: Ig kappa chain V region W3129 #status predicted <VAR>

Query Match 89.2%; Score 620; DB 2; Length 132;
Best Local Similarity 90.8%; Pred. No. 5,1e-51;
Matches 118; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 3 LPVRLVLLFWIPVSGGVVVTQTPLSPVSGDOVSICRSSQSLAKSYGNTYLSWYL 62

Db 2 LPVRLVLLFWIPVSGGVVVTQTPLSPVSGDOVSICRSSQSLATSHGITYLSWYL 61

Qy 63 HKPQSPQLLYGTSNRFSGVPDRFSGSGSTDTLKSTIKPKPDLMGYVYLGSTHQPRT 122

Db 62 HKPQSPQLLYGTSNRFSGVPDRFSGSGSTDTLKSTIKPKPDLMGYVYLGSTHQPRT 121

Qy 123 FGSGTKLEIK 132

Db 122 FGAGTKLEIK 131

RESULT 2

H30560
Ig kappa chain V region (36.1.2D) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 20-Mar-1998

C:Accession: H30560

R:Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989

A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono

A:Reference number: A30560; MUID:89110062

A:Accession: H30560

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAT>

A:Cross-References: GB:M24275; NID:g197085; PID:g197086
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 82.9%; Score 576; DB 2; Length 113;
Best Local Similarity 97.3%; Pred. No. 5.3e-47;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 21 DVVYQTPLSLPVSGDVSISCRSSQSLAKSYGNTYLSWYLRKPGSPOLLITIGISNRF 80
|||||
Db 1 DVVYQTPLSLPVSGDVSISCRSSQSLAKSYGNTYLSWYLRKPGSPOLLITIGISNRF 60

QY 81 SGVPRFSGSGGDTFTLKISTIKPEDLGMYCLOGTHQPYTFGGGTLEIK 132
|||||
Db 61 SGVPRFSGSGGDTFTLKISTIKPEDLGMYCLOGTHQPYTFGGGTLEIK 112

RESULT 3

E30560
Ig kappa chain V region (16.4.12E) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 16-Aug-1996

C:Accession: E30560

R:Matsumura, T.; Kabat, E.A.

J. Immunol. 142, 863-870, 1989

A:Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal

A:Reference number: A30560; MUID:89110062

A:Accession: E30560

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAT>

A:Note: the authors translated the codon GTA for residue 30 as His

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 82.6%; Score 574; DB 2; Length 113;
Best Local Similarity 97.3%; Pred. No. 8.1e-47;

Matches 109; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 21 DVVYQTPLSLPVSGDVSISCRSSQSLAKSYGNTYLSWYLRKPGSPOLLITIGISNRF 80
|||||
Db 1 DVVYQTPLSLPVSGDVSISCRSSQSLAKSYGNTYLSWYLRKPGSPOLLITIGISNRF 60

QY 81 SGVPRFSGSGGDTFTLKISTIKPEDLGMYCLOGTHQPYTFGGGTLEIK 132
|||||
Db 61 SGVPRFSGSGGDTFTLKISTIKPEDLGMYCLOGTHQPYTFGGGTLEIK 112

RESULT 4

E37203
Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S37203

R:Flischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.

submitted to the EMBL Data Library, August 1993

A:Description: Production and cloning of TMV-specific monoclonal antibodies.

A:Reference number: S37200

A:Accession: S37203

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 <FIS>

C:Cross-references: EMBL:X74588; NID:9402597; PID:e86056; PID:g1333980

C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 81.0%; Score 563; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 8.5e-46;

Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DVVYQTPLSLPVSGDVSISCRSSQSLAKSYGNTYLSWYLRKPGSPOLLITIGISNRF 80
|||||
Db 1 DVVYQTPLSLPVSGDVSISCRSSQSLAKSYGNTYLSWYLRKPGSPOLLITIGISNRF 60

QY 81 SGVPRFSGSGGDTFTLKISTIKPEDLGMYCLOGTHQPYTFGGGTLEIK 132
|||||
Db 61 SGVPRFSGSGGDTFTLKISTIKPEDLGMYCLOGTHQPYTFGGGTLEIK 112

RESULT 5
B39276
Ig light chain precursor V-D-J region (6-19) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 08-Sep-1997

C:Accession: B39276

R:Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izul, S.

Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990

A:Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis

A:Reference number: A39276; MUID:91088540

A:Accession: B39276

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-131 <REI>

A:Cross-references: GB:M55313; NID:g198095; PID:g198096

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 80.6%; Score 560.5; DB 2; Length 131;
Best Local Similarity 80.3%; Pred. No. 1.7e-45;

Matches 106; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPRLVLLFMTIPSSGDPVYVTPPLSLPVSGDVSISCRSSQSLAKSYGNTYLSW 60
|||||
Db 1 MKLPRLVLLFMTIPSSGDPVYVTPPLSLPVSGDVSISCRSSQSLAKSYGNTYLSW 59

QY 61 YLHRPGSPOLLITIGISNRFSGVPRFSGSGGDTFTLKISTIKPEDLGMYCLOGTHQ 120
|||||
Db 60 YLHRPGSPOLLITIKVSNRFGVPRFSGSGGDTFTLKISRVAEDLGYYFCQSGTHVP 119

QY 121 YTFGGGTLEIK 132
|||||
Db 120 YTFGGGTLEIK 131

RESULT 6

B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996

C:Accession: B34904; H34903

R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990

A:Title: Active site structure and antigen binding properties of idiotypically cross-

A:Reference number: A34903; MUID:90094387

A:Accession: B34904

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-131 <BED>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 79.6%; Score 553.5; DB 2; Length 131;
Best Local Similarity 80.3%; Pred. No. 7.7e-45;

Matches 106; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 MKLPRLVLLFMTIPSSGDPVYVTPPLSLPVSGDVSISCRSSQSLAKSYGNTYLSW 60
|||||
Db 1 MKLPRLVLLFMTIPSSGDPVYVTPPLSLPVSGDVSISCRSSQSLAKSYGNTYLSW 59

QY 61 YLHRPGSPOLLITIGISNRFSGVPRFSGSGGDTFTLKISTIKPEDLGMYCLOGTHQ 120
|||||
Db 60 YLHRPGSPOLLITIKVSNRFGVPRFSGSGGDTFTLKISRVAEDLGYYFCQSGTHVP 119

QY 121 YTFGGGTLEIK 132
|||||
Db 120 YTFGGGTLEIK 131

RESULT 7

C34904

Ig kappa chain precursor V region (3-24) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 13-Mar-1997
C:Accession: C34904; 131485
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-139, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-reactive kappa chain precursor V region
A:Reference number: A34903; M01D:90094387
A:Accession: C34904
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BE2>
R:Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A:Title: Comparison of variable region primary structures within an anti-fluorescein idiotype
A:Reference number: A31485; M01D:89109167
A:Accession: 131485
A:Status: preliminary
A:Molecule type: protein
A:Residues: 20-52 <BE2>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 79.1%; Score 549.5; DB 2; Length 131;
Best Local Similarity 79.5%; Pred. No. 1.8e-44;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;
Db 1 MKLPVRLVLLFWIPVSGDGVVVTQPLSLPVSFQDVYSICRSSQSLAKSYGNTYLSW 60
1 MKLPVRLV-LFWIPVSSSDVVMQTQPLSLPVSLDQASISCRSSQSLVHSGNTYLSW 59
QY 61 YLHKPGSPQLLYIGISNRPSSGVPDRFSGSGSTDTFTLKSTIKPEDLGMYTCLOGTROP 120
Y 60 YLQKPGSPQLLYIKVSNRSGVPDRFSGSGSTDTFTLKSRVADLDGYFCQSOSTHPV 119
Db 121 YTFGGGTKEIK 132
Y 120 WTFGGGTKEIK 131

RESULT 8
PLOT202
anti-DNA autoantibody BV16-13, kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-May-1996
C:Accession: P10202
R:Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N
A:Reference number: P10198
A:Accession: P10202
A:Molecule type: mRNA
A:Residues: 1-114 <SM1>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
F:24-39/Region: complementarity-determining 1
F:55-61/Region: complementarity-determining 2
F:94-103/Region: complementarity-determining 3
F:102-114/Region: JH region

Query Match 78.9%; Score 548.5; DB 2; Length 114;
Best Local Similarity 94.7%; Pred. No. 1.9e-44;
Matches 107; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
QY 21 DVAVTQPLSLPVSFQDVYSICRSSQSLAKSYGNTYLSWYLRKPGSPQLLYIGISNRF 80
Y 20 DVAVTQPLSLPVSFQDVYSICRSSQSLAKSYGNTYLSWYLRKPGSPQLLYIGISNRF 80
Db 1 DVAVTQPLSLPVSFQDVYSICRSSQSLAKSYGNTYLSWYLRKPGSPQLLYIGISNRF 60
QY 81 SGVPDRFSGSGSTDTFTLKSTIKPEDLGMYTCLOGTROP-YTFGGGTKEIK 132
Y 80 SGVPDRFSGSGSTDTFTLKSTIKPEDLGMYTCLOGTROP-YTFGGGTKEIK 132
Db 61 SGVPDRFSGSGSTDTFTLKSTIKPEDLGMYTCLOGTROP-YTFGGGTKEIK 113

RESULT 9
B32513
Ig kappa chain precursor V region (MRL14) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 20-Mar-1998
C:Accession: B32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization a
A:Reference number: A94689; M01D:88331384
A:Accession: B32513
A:Molecule type: DNA
A:Residues: 1-131 <KOF>
A:Cross-references: GB:M20828; NID:9196937; PID:9196938
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 78.6%; Score 546.5; DB 2; Length 131;
Best Local Similarity 79.5%; Pred. No. 3.4e-44;
Matches 105; Conservative 8; Mismatches 18; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDGVVVTQPLSLPVSFQDVYSICRSSQSLAKSYGNTYLSW 60
Y 1 MKLPVRLV-LFWIPVSSSDVVMQTQPLSLPVSLDQASISCRSSQSLVHSGNTYLSW 59
Db 1 MKLPVRLV-LFWIPVSSSDVVMQTQPLSLPVSLDQASISCRSSQSLVHSGNTYLSW 59
QY 61 YLHKPGSPQLLYIGISNRPSSGVPDRFSGSGSTDTFTLKSTIKPEDLGMYTCLOGTROP 120
Y 60 YLQKPGSPQLLYIKVSNRSGVPDRFSGSGSTDTFTLKSRVADLDGYFCQSOSTHPV 119
Db 121 YTFGGGTKEIK 132
Y 120 YTFGGGTKEIK 131

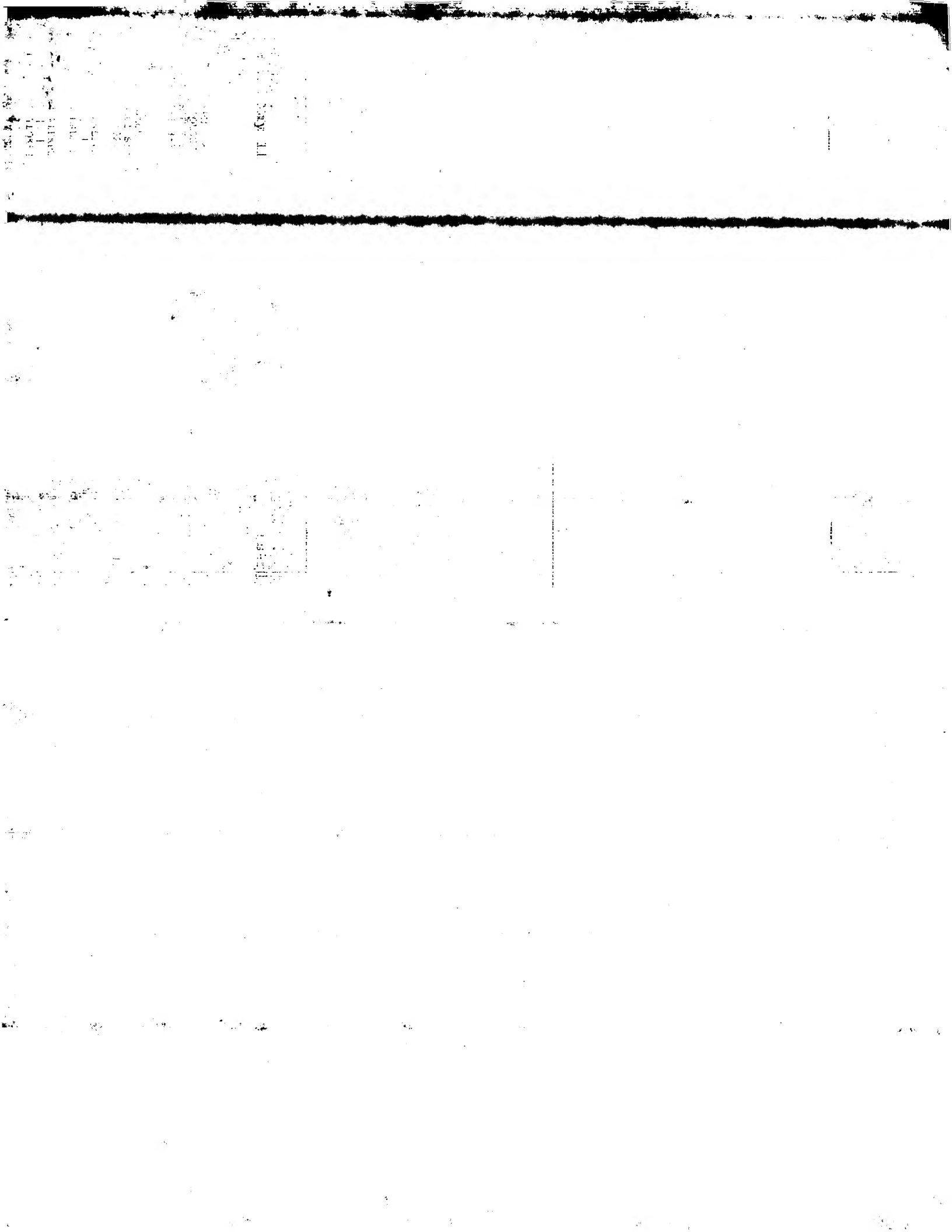
RESULT 10
B30577
Ig kappa chain precursor V region (MRL10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
C:Accession: B30577
R:Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Th
J. Exp. Med. 161, 805-815, 1985
A:Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r
A:Reference number: A30577; M01D:85159423
A:Accession: B30577
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <KOF>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 78.6%; Score 546.5; DB 2; Length 131;
Best Local Similarity 79.5%; Pred. No. 3.4e-44;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDGVVVTQPLSLPVSFQDVYSICRSSQSLAKSYGNTYLSW 60
Y 1 MKLPVRLV-LFWIPVSSSDVVMQTQPLSLPVSLDQASISCRSSQSLVHSGNTYLSW 59
Db 1 MKLPVRLV-LFWIPVSSSDVVMQTQPLSLPVSLDQASISCRSSQSLVHSGNTYLSW 59
QY 61 YLHKPGSPQLLYIGISNRPSSGVPDRFSGSGSTDTFTLKSTIKPEDLGMYTCLOGTROP 120
Y 60 YLQKPGSPQLLYIKVSNRSGVPDRFSGSGSTDTFTLKSRVADLDGYFCQSOSTHPV 119
Db 121 YTFGGGTKEIK 132
Y 120 YTFGGGTKEIK 131
RESULT 11
D34904

A:Accession: P50074
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-111 <LEV>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 77.3%; Score 537.5; DB 2; Length 111;
 Best Local Similarity 92.9%; Pred. No. 2e-43;
 Matches 104; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
 QY 21 DVVVTQTPLSLPVSGDQVSISCRSSQSLAKSYGNTYLSWYLRKPGQSPOLLTYGISNRF 80
 Db 1 DVVVTQTPLSLPVSGDQVSISCRSSQSLANSYGNLYLSWYLRKPGQSPOLLTYGISNRF 60
 QY 81 SGVPRFSGSGSDFTLKISTIKPEDLGWYCIQGTHTQPTFGGKLEIK 132
 Db 61 SGVPRFSGSGSDFTLKISTIKPEDLGWYCIQGTHTQ-LTFGAGKLEIK 111

Search completed: May 11, 1999, 12:23:24
 Job time: 297 sec



RA NOVOTNY J., MARGOLIES M.N.;
 RL BIOCHEMISTRY 22:1153-1158(1983).
 CC -1- THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT
 CC BINDS DIOXIN.
 DR HSP: A01914; KMS26.
 DR HSP: P01607; IIG1.
 KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY; HYBRIDOMA.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 39 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 54 FRAMEWORK 2.
 FT DOMAIN 4 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 61 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 6 62 COMPLEMENTARITY-DETERMINING 4.
 FT DOMAIN 7 103 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12273 MW; 58372CBE CRC32;

Query Match 67.8%; Score 471; DB 1; Length 113;
 Best Local Similarity 80.4%; Pred. No. 2,76-40;
 Matches 90; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

OY 21 DVTVTOTPLSPVSEFGDVSISCRSSGSLAKSYGNTYLSYTLKRGSPOLLITIGISNR 80
 DB 1 DVTVTOTPLSPVSEFGDVSISCRSSGSLAKSYGNTYLSYTLKRGSPOLLITIGISNR 80

OY 81 SGVDRSGSGSGDTFTLKSTIKPEDGMVYCYLOGTHQHYTFGGGKLEIK 132
 DB 61 SGVDRSGSGSGDTFTLKSTIKPEDGMVYCYLOGTHQHYTFGGGKLEIK 112

RESULT 3
 KV2A_HUMAN ID KV2A_HUMAN STANDARD; PRT; 117 AA.
 AC P06309;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-II REGION (GM607) (FRAGMENT).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX KLOBECK H.G.; SOLOMON A.; ZACHAU H.G.;
 RL NATURE 309:73-76(1984).
 DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
 DR PIR; A01889; K2HUGM.
 DR HSP; P01679; ICBV.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT NON TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION (GM607).
 FT DOMAIN 1 27 FRAMEWORK 1.
 FT DOMAIN 2 43 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 44 58 FRAMEWORK 2.
 FT DOMAIN 4 59 65 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 66 97 FRAMEWORK 3.
 FT DOMAIN 6 98 106 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 7 107 116 FRAMEWORK 4.
 FT DISULFID 27 97 BY SIMILARITY.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12664 MW; E09E9ACC CRC32;

Query Match 60.7%; Score 422; DB 1; Length 117;
 Best Local Similarity 71.3%; Pred. No. 2,16-35;
 Matches 82; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

OY 18 SGDDVVTOTPLSPVSEFGDVSISCRSSGSLAKSYGNTYLSYTLKRGSPOLLITIGIS 77
 DB 18 SGDDVVTOTPLSPVSEFGDVSISCRSSGSLAKSYGNTYLSYTLKRGSPOLLITIGIS 77

DB 2 SSGDIVTOSPLSPVTPGPASISCRSSGSLAKSYGNTYLSYTLKRGSPOLLITIGIS 61
 OY 78 NRSFGVDRSGSGSGDTFTLKSTIKPEDGMVYCYLOGTHQHYTFGGGKLEIK 132
 DB 62 NRSFGVDRSGSGSGDTFTLKSTIKPEDGMVYCYLOGTHQHYTFGGGKLEIK 116

RESULT 4
 KV2D_HUMAN ID KV2D_HUMAN STANDARD; PRT; 113 AA.
 AC P01617;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (TEW).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE (BENCE-JONES PROTEIN TEW).
 RX MEDLINE; 74148480.
 RA PUTNAM F.W.; WHITLEY E.J. JR., PAUL C., DAVIDSON J.N.;
 RL BIOCHEMISTRY 12:3763-3780(1973).
 RN [2]
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
 RX MEDLINE; 73166638.
 RA TERRY W.D., PAGE D.L., KIMURA S., ISOBE T., OSSEMAN E.F.,
 RA GLENNER G.G.;
 RL J. CLIN. INVEST. 52:1276-1281(1973).
 CC -1- THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE
 CC -1- JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
 CC -1- THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH
 CC PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 DR PIR; A01888; K2HUTV.
 DR HSP; P01679; ICBV.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; AMYLOID.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 39 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 40 54 FRAMEWORK 2.
 FT DOMAIN 4 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 62 93 FRAMEWORK 3.
 FT DOMAIN 6 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 7 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12316 MW; FC2B2819 CRC32;

Query Match 60.1%; Score 418; DB 1; Length 113;
 Best Local Similarity 69.6%; Pred. No. 5e-35;
 Matches 78; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

OY 21 DVTVTOTPLSPVSEFGDVSISCRSSGSLAKSYGNTYLSYTLKRGSPOLLITIGISNR 80
 DB 1 DVTVTOTPLSPVTPGPASISCRSSGSLAKSYGNTYLSYTLKRGSPOLLITIGISNR 60

OY 81 SGVDRSGSGSGDTFTLKSTIKPEDGMVYCYLOGTHQHYTFGGGKLEIK 132
 DB 61 SGVDRSGSGSGDTFTLKSTIKPEDGMVYCYLOGTHQHYTFGGGKLEIK 112

RESULT 5
 KV2A_HUMAN ID KV2A_HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (CDM).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.

Query Match	56.98;	Score 395.5;	DB 1;	Length 112
Best Local Similarity	65.28;	Pred. No. 8.5e-33;		

RESULT	11			
KVZF_MOUSE				
ID	KVZF_MOUSE	STANDARD:	PRT:	113 AA.
AC	P01630:			
DT	21-JUL-1986	(REL. 01, CREATED)		
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)		
DT	01-OCT-1993	(REL. 27, LAST ANNOTATION UPDATE)		
DE	IG KAPPA CHAIN V-II REGION (7534.1).			
OS	MUS MUSCULUS (MOUSE).			
CC	EUMAROTEA, MEALAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUATHERIA, RODENTIA.			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE: 83256427.			
RA	CHANG J.-Y., HERBST H., AEBERSOLD R., BRAUN D.G.,			
RL	BIOCHEM. J. 211:173-180(1983).			

OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041854.
 RA MARSH P., MILLS F., GOULD H.;
 RL NUCLEIC ACIDS RES. 13:6531-6544(1985).
 RN [2]
 RP REVISION TO 76.
 RA MARSH P.;
 RL SUBMITTED (OCT-1986) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: X02990; G37910; -
 DR PIR: A01905; KAHU17.
 DR HSSP: P01607; 21MN.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-III REGION (B17).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 133 FRAMEWORK 4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 134 134
 SQ SEQUENCE 134 AA; 14966 MW; BB63E06A CRC32;

Query Match 55.5%; Score 385.5; DB 1; Length 134;
 Best Local Similarity 57.1%; Pred. No. 1e-31;
 Matches 76; Conservative 23; Mismatches 33; Indels 1; Gaps 1;

QY 1 MKLPRLVLLFWIPVSGGDVVTOTPLSPVSGDQVSISCRSSQSLAKSYGNTYLS 59
 1 MVLQTOYFISLLMISGAYGDIWMTQSPDSLAVSGERATINCCKSSQSLVSSDNKNYLA 60
 DB 60 WYLRPGSPOLLIGYISNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYTCLOGTHQ 119
 61 WYQKRGSPRLIYDASSRANGIPDRFSGSGGTDFTLISRLPEDEFAVYYCQYSTSP 120
 DB 120 PYRGGGTRKLEIK 132
 121 PWTFGGGTRKLEIK 133

RESULT 15
 KV3K HUMAN
 ID KY3K HUMAN STANDARD; PRT: 128 AA.
 AC P06311;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 RA KLOBECK H.G., MEINDL A., COMBRIANO G., SOLOMON A., ZACHAU H.G.;
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
 DR EMBL: Z00021; G33179; -
 DR PIR: A01899; K3HU41.
 DR HSSP: P01607; 3HEM.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 128
 FT DOMAIN 21 43 IG KAPPA CHAIN V-III REGION (IARC/BL41).
 FT DOMAIN 44 54 FRAMEWORK 1.
 FT DOMAIN 55 69 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 70 76 FRAMEWORK 2.
 FT DOMAIN 77 108 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 109 117 FRAMEWORK 3.
 FT DOMAIN 117 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 118 128 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 128 128
 SQ SEQUENCE 128 AA; 14070 MW; 318E08AF CRC32;

Query Match 54.7%; Score 380.5; DB 1; Length 128;
 Best Local Similarity 55.3%; Pred. No. 3.1e-31;
 Matches 73; Conservative 26; Mismatches 28; Indels 5; Gaps 1;

QY 1 MKLPRLVLLFWIPVSGGDVVTOTPLSPVSGDQVSISCRSSQSLAKSYGNTYLSW 60
 1 MVLQTOYFISLLMISGAYGDIWMTQSPDSLAVSGERATINCCKSSQSLVSSDNKNYLA 60
 DB 61 WYLRPGSPOLLIGYISNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYTCLOGTHQ 120
 56 WYQKRGSPRLIYDASSRANGIPDRFSGSGGTDFTLISRLPEDEFAVYYCQYSTSP 115
 QY 121 PYRGGGTRKLEIK 132
 121 PWTFGGGTRKLEIK 127

Search completed: May 11, 1999, 12:20:08
 Job time: 305 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:16:48 ; Search time 38.54 Seconds

(without alignments)
188,955 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence: 1 MLLPVLVLLLEFVPSGG.....CLOGTHQPYTGGGTRLEIK 132

Scoring table: BLOSUM62

Searched: 180763 seqs, 55169189 residues

Database :

SPREMBL-8:*
1: sp_fungi:*
2: sp_human:*
3: sp_invertebrate:*
4: sp_mammal:*
5: sp_mhc:*
6: sp_organelle:*
7: sp_phage:*
8: sp_plant:*
9: sp_bacteria:*
10: sp_rodent:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_unclassified:*
14: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	371	45.3	100	2	Q15535	015535 homo sapien
2	315	45.3	130	10	P80913	P80913 mus musculu
3	148	21.3	513	10	P97797	P97797 mus musculu
4	146	20.7	509	10	O08907	O08907 mus musculu
5	144	20.7	509	10	O35924	O35924 mus musculu
6	137	19.7	509	10	O88555	O88555 mus musculu
7	137	19.7	291	10	O88556	O88556 mus musculu
8	134.5	19.4	50	2	Q15533	Q15533 homo sapien
9	132.5	19.1	132	5	Q11175	Q11175 mus musculu
10	129.5	18.6	145	2	Q16337	Q16337 homo sapien
11	129.5	18.6	135	5	Q31174	Q31174 mus musculu
12	126.5	18.2	133	10	O61243	O61243 mus musculu
13	125.5	18.1	210	4	P79336	P79336 felis silve
14	119.5	17.2	509	10	P97710	P97710 rattus norv
15	115.5	16.6	418	10	O70426	O70426 rattus norv
16	112	16.1	134	5	Q31180	Q31180 mus musculu
17	109.5	15.8	135	2	Q99602	Q99602 homo sapien
18	109	15.7	133	5	Q31178	Q31178 mus musculu
19	105.5	15.2	132	5	Q31177	Q31177 mus musculu
20	104.5	15.0	401	4	O08835	O08835 ceropithe
21	104	15.0	401	4	O46632	O46632 bos taurus
22	104	15.0	137	5	Q31181	Q31181 mus musculu
23	102	14.7	372	2	Q15267	Q15267 homo sapien
24	102	14.7	364	2	Q15268	Q15268 homo sapien
25	100.5	14.5	118	5	Q31176	Q31176 mus musculu
26	99.5	14.3	228	10	O70153	O70153 rattus norv
27	98.5	14.2	254	12	O90557	O90557 ginglymosto
28	97.5	14.0	503	2	P78324	P78324 homo sapien
29	97.5	14.0	117	5	Q31278	Q31278 rattus norv

30	97	14.0	198	2	Q13970	Q13970 homo sapien
31	97	14.0	506	4	O46631	O46631 bos taurus
32	97	14.0	157	12	O90539	O90539 ginglymosto
33	96	13.8	158	12	O90531	O90531 ginglymosto
34	94	13.5	252	12	O90568	O90568 ginglymosto
35	92.5	13.3	398	2	O00241	O00241 homo sapien
36	92.5	13.3	119	2	O99599	O99599 homo sapien
37	92.5	13.3	121	2	O99600	O99600 homo sapien
38	91	13.1	213	5	Q31127	Q31127 mus musculu
39	91	13.1	133	12	O90553	O90553 ginglymosto
40	90.5	13.0	113	12	O90552	O90552 ginglymosto
41	90.5	13.0	145	12	O90555	O90555 ginglymosto
42	90.5	13.0	250	12	O90569	O90569 ginglymosto
43	89.5	12.9	268	12	O90524	O90524 ginglymosto
44	89	12.8	139	12	O90533	O90533 ginglymosto
45	88.5	12.7	1021	2	Q15856	Q15856 homo sapien

ALIGNMENTS

RESULT	1	ALIGNMENTS
ID	Q15535	PRELIMINARY; PRT; 100 AA.
AC	Q15535;	
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)	
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT	01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)	
DE	V KAPPA (FRAGMENT).	
OS	HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;	
OC	CATARRHINI; HOMINIDAE; HOMO.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	KATO S., TACHIBANA K., TAKAYAMA N., KATAOKA H., YOSHIDA M.C.,	
RA	TAKANO T.;	
RL	SUBMITTED (SEP-1990) TO EMBL/GENBANK/DBJ DATA BANKS.	
DR	EMBL; D90161; G1262585; -	
DR	PFAM; PF00047; 1g; 1.	
FT	NON_TER 1 1	
FT	NON_TER 100 100	
SQ	SEQUENCE 100 AA; 10871 MW; 06A1440D CRC32;	
Query Match 53.4%; Score 371; DB 2; Length 100;		
Best Local Similarity 72.0%; Pred. No. 3.6e-28;		
Matches 72; Conservative 10; Mismatches 18; Indels 0; Gaps 0;		
QY	21 DVTVTQPLSLPVSPFGDVVISGRSSQSLAKSYGNTYLSWYLRPGSPQQLLYGISNRF 80	
DB	1 DVTWQTPPLSLVTPGPGPASISCKSIQSLHSDGKTYLYXLRPGSPQQLLYEVSRRF 60	
QY	81 SGVPRFSGSGSGTDFLTAKISTIKPEDLGWYICLOGTHOP 120	
DB	61 SGVPRFSGSGSGTDFLTAKISRVKAEADVGYCYMCQGHLP 100	
RESULT 2		
ID	P80913	PRELIMINARY; PRT; 130 AA.
AC	P80913;	
DT	01-NOV-1998 (TREMBLREL. 08, CREATED)	
DT	01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)	
DT	01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)	
DE	US KAPPA CHAIN V REGION PRECURSOR.	
OS	MUS MUSCULUS (MOUSE).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;	
OC	SCIUROGNATHI; MURIDAE; MORINAE; MUS.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	JANON K.;	
RL	SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.	
DR	EMBL; X79906; E269393; ALT_TERM.	


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Db 15 LCLLLSASCFCCTGATGTEKVTQPEKSVSVAGDSTILNCTVTSLLPVG---PIRW- 70
Oy 63 HRPQSPOLLIVGISN---RFSGVDRFSGSGSDTFLTKSTIKPEDLGMYCL--Q 115
    ||| ||| | : : : | : : : | : : : | : : : | : : : | : : : |
Db 70 RGVGS-RLIIVSFTGHEHFRVNVSD--TTKNNMDFSRISNVTPEDAGTYCVKFOR 126
Oy 116 GTHQPT---FGGKTKLEI 131
    | : | | | | | : : : | : : : |
Db 127 GSSEPDTEIOSGGGTEYV 145

RESULT 5
O35924 PRELIMINARY; PRT; 509 AA.
ID 035924;
AC 035924;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1, PRECURSOR...
DE (P84).
GN PTNSL.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MORIDAE; MORINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98012243.
RA LAGEAUD C.F., NARAYANAN V.;
RT "The murine p84 neural adhesion molecule is SHPS-1, a member of the
RT phosphatase-binding protein family.";
RL J. NEUROSCI. 17:8702-8710(1997).
DR EMBL; U89694; G2580535;
DR MGI; MGI:108563; PTNSL.
DR PFAM; PF00047; 19; 3.
KW SIGNAL.
FT SIGNAL. 1 31 POTENTIAL.
FT CHAIN 32 509 P84.
SQ SEQUENCE 509 AA; 56056 MW; 3A781050 CRC32;

Query Match 20.7%; Score 144; DB 10; Length 509;
Best Local Similarity 33.1%; Pred. No. 4.3e-06;
Matches 46; Conservative 24; Mismatches 47; Indels 22; Gaps 8;

Oy 7 LTVLL-----FWIPVSGGVVYQTPLSPVSGDOVISICRSGSLAKSYGNTYISWYL 62
    ||| | | | | : : : | : : : | : : : | : : : | : : : |
Db 15 LCLLLSASCFCCTGATGTEKVTQPEKSVSVAGDSTVLCITLSLPVG---PIRW- 70
Oy 63 HRPQSPOLLIVGISN---RFSGVDRFSGSGSDTFLTKSTIKPEDLGMYCL--Q 115
    ||| ||| | : : : | : : : | : : : | : : : | : : : |
Db 70 RGVGS-RLIIVSFTGHEHFRVNVSD--TTKNNMDFSRISNVTPEDAGTYCVKFOR 126
Oy 116 GTHQPT---FGGKTKLEI 131
    | : | | | | | : : : | : : : |
Db 127 GSSEPDTEIOSGGGTEYV 145

RESULT 6
O88555 PRELIMINARY; PRT; 509 AA.
ID 088555;
AC 088555;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE INHIBITORY RECEPTOR SHPS-1 LONG ISOFORM.
GN SHPS1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=THYMUS;
DE STRAIN=C57BL/6; TISSUE=THYMUS;

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RA VEILLETTE A., THIBAUDEAU E., LATOUR S.;
RT "High expression of inhibitory receptor SHPS-1 and its association
RT with protein tyrosine phosphatase SHP-1 in macrophages.";
RL J. BIOL. CHEM. 0:0-0(1998).
DR EMBL; AF072543; G3273916;
SQ SEQUENCE 509 AA; 55986 MW; 3AF9E651 CRC32;

Query Match 19.7%; Score 137; DB 10; Length 509;
Best Local Similarity 31.4%; Pred. No. 2e-05;
Matches 44; Conservative 25; Mismatches 47; Indels 24; Gaps 8;

Oy 7 LTVLL-----FWIPVSGGVVYQTPLSPVSGDOVISICRSGSLAKSYGNTYISWYL 62
    ||| | | | | : : : | : : : | : : : | : : : | : : : |
Db 15 LCLLLSASCFCCTGATGTEKVTQPEKSVSVAGDSTVLCITLSLPVG---PIRW- 70
Oy 63 HRPQSP-OLLIVGISN---RFSGVDRFSGSGSDTFLTKSTIKPEDLGMYCL--Q 115
    ||| ||| | : : : | : : : | : : : | : : : | : : : |
Db 70 --RGVPSRLIIVSFTGHEHFRVNVSD--TTKNNMDFSRISNVTPADAGIYCVKFOR 125
Oy 115 OGTHQPT---FGGKTKLEI 131
    | : | | | | | : : : | : : : |
Db 126 KGSSEPDTEIOSGGGTEYV 145

RESULT 8
O15533 PRELIMINARY; PRT; 50 AA.
ID 015533;
AC 015533;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE DNA REARRANGED BY A T(2;8) TRANSLOCATION LEADING TO BURKITT'S LYMPHOMA
DE

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Query Match      19.1% Score 132.5 DB 5 Length 132
Best Local Similarity 32.6% Pred. NO. 1.3e-05
Matches 42; Conservative 22; Mismatches 54; Indels 11; Gaps

QY      8 LVLLFWIPSGDVVYQTPLSPVSRGDVYSICRSSSLAKSYGNTYLSWTLHRPGQ 67
      : : : : : | | | | | : : : : : | | | | | :
Db       7 VAVILLIGRHHG-SVYQTEGQVTVESKSLINCTYS--ATSIQYPLNFWVRVRI 62
      : : : : : | | | | | : : : : : | | | | | :

QY      68 SPOLLIGISNRFSFGVDPRESC--SGSDTDLTALKISTIKPEDLGMYCL---QSTHPY 122
      : : : : : | | | | | : : : : : | | | | | :
Db       63 GPOLLIVITAGORSSRGFEATYNKEATSPHLAKASVOESDSAVYYCALRNSGYO--R 120
      : : : : : | | | | | : : : : : | | | | | :

QY      123 FGGGTGKLEI 131
      | | | | | :

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Query Match	18.68;	Score 129.5;	DB 5;	Length 135;
Best Local Similarity	29.08;	Pred. NO. 2.5e-05;		

KM SIGNAL; TRANSMEMBRANE; ALTERNATIVE SPLICING; IMMUNOGLOBULIN FOLD;
KW GLYCOPROTEIN; SH3-BINDING; PHOSPHORYLATION.
FT SIGNAL 1 26
FT CHAIN 27 509 SHP SUBSTRATE-1.
FT DOMAIN 28 373 EXTRACELLULAR (POTENTIAL).
FT TRANSFER 374 394 POTENTIAL.
FT DOMAIN 395 509 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 51 125 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 168 234 IG-LIKE C1-TYPE DOMAIN.
FT DOMAIN 270 336 IG-LIKE C1-TYPE DOMAIN.
FT DOMAIN 436 439 SH2-BINDING (POTENTIAL).
FT DOMAIN 446 451 SH3-BINDING (POTENTIAL).
FT DOMAIN 460 463 SH2-BINDING (POTENTIAL).
FT DOMAIN 477 480 SH2-BINDING (POTENTIAL).
FT DOMAIN 501 504 SH2-BINDING (POTENTIAL).
FT MOD_RES 436 436 SH2-BINDING (POTENTIAL).
FT MOD_RES 460 460 POTENTIAL.
FT MOD_RES 477 477 POTENTIAL.
FT MOD_RES 501 501 POTENTIAL.
FT CARBOHYD 54 54 POTENTIAL.
FT CARBOHYD 93 93 POTENTIAL.
FT CARBOHYD 169 169 POTENTIAL.
FT CARBOHYD 181 181 POTENTIAL.
FT CARBOHYD 203 203 POTENTIAL.
FT CARBOHYD 209 209 POTENTIAL.
FT CARBOHYD 242 242 POTENTIAL.
FT CARBOHYD 246 246 POTENTIAL.
FT CARBOHYD 271 271 POTENTIAL.
FT CARBOHYD 293 293 POTENTIAL.
FT CARBOHYD 312 312 POTENTIAL.
FT CARBOHYD 320 320 POTENTIAL.
FT CARBOHYD 345 345 POTENTIAL.
FT CONFLICT 162 162 G -> A (IN REF. 2 AND 3).
SQ SEQUENCE 509 AA; 55690 MM; 6D940097 CRC32;

Query Match 17.2%; Score 119.5; DB 10; Length 509;
Best Local Similarity 30.4%; Pred. No. 0.00086;
Matches 42; Conservative 22; Mismatches 55; Indels 19; Gaps 7;

OY 7 LVLVLL---FWIPVSGDVVVTQPLSLPVSFGDQVSISSRSQSLAKSYGNTYLSWYL 62
DB 15 LFCILLASCFACAGASGKELKVTQADKSVSAAGDSATLNCVSSLPVPG---PIKWK 70
OY 63 HK-PGOSPOLLITIGISN--RFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYYCL---QG 116
DB 71 GEGONRSPPIYSFIDGEHPRITNVS--ATKRNMDPISICISNVTPEAGTYCYVKFKG 128
OY 117 THOPTY---FGGKTKLEI 131
DB 129 IVEPDTIKSGGGTTLTV 146

RESULT 15
070426 PRELIMINARY; PRT; 418 AA.

AC 070426; 070426; 070426; 070426; 070426; 070426; 070426; 070426; 070426; 070426;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE SIGNAL REGULATORY PROTEIN ALPHA (FRAGMENT).
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
NC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WAG/RIJ;
RA ADAMS S., VAN DER LAAN L.J.W., VERNON-WILSON E.,
RA RENADEL DE LAVALLETTE C., DOPP E.A., DIKSTRA C., SIMMONS D.L.,
RA VAN DEN BERG T.K.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF055065; G3170529; --
FT NON_TER 418 418

SQ SEQUENCE 418 AA; 45297 MM; 752D2171 CRC32;

Query Match 16.6%; Score 115.5; DB 10; Length 418;
Best Local Similarity 29.7%; Pred. No. 0.0017;
Matches 41; Conservative 24; Mismatches 54; Indels 19; Gaps 7;

OY 7 LVLVLL---FWIPVSGDVVVTQPLSLPVSFGDQVSISSRSQSLAKSYGNTYLSWYL 62
DB 14 LFCILLASCFACAGASGKELKVTQADKSVSAAGDSATLNC---IVCSILTPVGPWK 69
OY 63 HK-PGOSPOLLITIGISN--RFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYYCL---QG 116
DB 70 GEGONRSPPIYSFIDGEHPRITNVS--ATKRNMDPISICISNVTPEAGTYCYVKFKG 127
OY 117 THOPTY---FGGKTKLEI 131
DB 128 IVEPDTIKSGGGTTLTV 145

Search completed: May 11, 1999, 12:21:01
Job time: 253 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 11:39:53 ; Search time 44.09 Seconds

(Without alignments)
60.552 Million cell updates/sec

Title: us-08-700-737-12

Perfect score: 695

Sequence: 1 MKLPVRLVLLFWIPVSGG.....CIQGTHTQPTFGGKLEIK 132

Scoring table: BLOSUM62

Searched: 162890 seqs, 20225328 residues

Database: A_Geneseq_34.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	695	100.0	132	1	Murine Act-1 light
2	695	100.0	140	1	Consensus protein
3	608	87.5	138	1	Light chain of a h
4	559.5	80.5	238	1	3F4 Human IgG4 exp
5	559.5	80.5	238	1	Murine anti-porcine
6	558.5	80.4	131	1	Variable kappa cha
7	554.5	79.8	149	1	Anti-Idiotypic mono
8	548.5	78.9	131	1	Murine KC-4 immuno
9	548.5	78.9	131	1	Murine KC-4 immuno
10	548.5	78.9	131	1	Chimeric Mab light
11	543.5	78.2	131	1	BR55-2 murine IgG3
12	543.5	77.3	131	1	Humanised murine K
13	537.5	77.3	131	1	Humanised murine K
14	537.5	77.3	131	1	Humanised murine K
15	537.5	77.3	131	1	Humanised murine K
16	535.5	77.1	238	1	L chain subunit of
17	535.5	77.1	132	1	Variable region of
18	535.5	77.1	238	1	Anti-human Fas mon
19	529.5	76.2	140	1	Variable light cha
20	527.5	75.9	172	1	R6-5-D6 anti-ICAM-
21	523	75.3	150	1	Murine monoclonal
22	519.5	74.7	131	1	Murine BRE-3 immu
23	519.5	74.7	131	1	Murine BRE-3 immu
24	517.5	74.5	131	1	Co-1 Light Chain V
25	517.5	74.5	131	1	Mab Co-1 light cha
26	513	73.8	127	1	Murine ICR-8.1 V-K
27	513	73.8	127	1	Murine antibody IC
28	511.5	73.6	131	1	Humanised murine B
29	509	73.2	132	1	Amino acid sequenc
30	506.5	72.9	173	1	Murine anti-ICAM m
31	503	72.4	239	1	Anti-human Fas hum
32	503	72.4	239	1	Anti-human Fas hum
33	500	71.9	239	1	Anti-Fas Mab CH11
34	499	71.8	239	1	Anti-human Fas hum
35	499	71.8	239	1	Anti-human Fas hum
36	495	71.2	249	1	pSCFVNO11 encoding
37	489	70.4	249	1	Biosynthetic antiB
38	488.5	70.3	219	1	h66-118/h13-65/11-
39	485	69.8	135	1	Sequence of the VL
40	485	69.8	135	1	Monoclonal antibody
41	485	69.8	135	1	Monoclonal antibody
42	483	69.2	115	1	Light chain variab
43	481	69.2	263	1	Om212 single chain

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description
44	481	69.2	246	1	R27245	Sequence of the AA
45	481	69.2	110	1	R38159	Sequence of the 11

Query Match	Score	DB 1	Length	132
Best Local Similarity	100.0%	Pred. No. 1.1e-49	Indels	0
Matches 132	Conservative	0	Mismatches	0
QY	1	MKLPVRLVLLFWIPVSGGDDVVTQPLSLPVSFGQVSISSRSSQSLAKSGYNTLSW	60	
DB	1	MKLPVRLVLLFWIPVSGGDDVVTQPLSLPVSFGQVSISSRSSQSLAKSGYNTLSW	60	
QY	61	YLHRPGSPOLLTYGISNRSFGVDFRSGSGGDTFTLKISTIKPEDLGMYYCLQGTROP	130	
DB	61	YLHRPGSPOLLTYGISNRSFGVDFRSGSGGDTFTLKISTIKPEDLGMYYCLQGTROP	130	
QY	121	YTFGGGKLEIK 132		
DB	121	YTFGGGKLEIK 132		

RESULT 2
ID W53817 standard; Protein; 140 AA.
AC W53817;
DT 14-JUL-1998 (first entry)

DE Consensus protein sequence of the murine variable light chain region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KM Muscosal addressin cell adhesion molecule-1; MadCAM-1;
 KM humanised antibody; murine antigen binding region; inhibition;
 KM leukocyte infiltration of tissue; treatment; inflammatory disease;
 KM inflammatory bowel disease.
 OS Mus sp.
 FH Key
 FT Peptide
 FT Protein
 FT 1. .20
 FT /note- "signal peptide"
 FT 21. .140
 FT /note- "mature protein"
 PN W09806248-A2.
 PD 19-FEB-1998.
 PR 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI; 98-159172/14.
 DR N-PSDB; V20086.
 PT Humanised immunoglobulin reactive with alpha4-beta7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 3; 145pp; English.
 CC The present sequence represents the consensus amino acid sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse light chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal addressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in muscosal
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20083-84. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 140 AA;

Query Match 100.0%; Score 695; DB 1; Length 140;
 Best Local Similarity 100.0%; Pred. No. 1.2e-49;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGGVVYTORPLSPVSGDVSISCRSSOSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGGVVYTORPLSPVSGDVSISCRSSOSLAKSYGNTYLSW 60
 QY 61 YLHAPGSPOLLIIYGISNRFSGVDPDRFSGSGSDFTIKITIKPEDIGMYTCLOGTHOP 120
 DB 61 YLHAPGSPOLLIIYGISNRFSGVDPDRFSGSGSDFTIKITIKPEDIGMYTCLOGTHOP 120
 QY 121 YTFGGGTRLEIK 132
 DB 121 YTFGGGTRLEIK 132

RESULT 3
 W53812
 ID W53812 standard; Protein; 138 AA.
 AC W53812;
 DT 14-JUL-1998 (first entry)
 DE Light chain of a humanised murine Act-1 antibody.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KM Muscosal addressin cell adhesion molecule-1; MadCAM-1;
 KM humanised antibody; murine antigen binding region; inhibition;
 KM leukocyte infiltration of tissue; treatment; inflammatory disease;

KW Inflammatory bowel disease.
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 FH Key
 FT Peptide
 FT Protein
 FT 1. .20
 FT /note- "signal peptide"
 FT 21. .138
 FT /note- "mature protein"
 PN W09806248-A2.
 PD 19-FEB-1998.
 PR 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI; 98-159172/14.
 DR N-PSDB; V20075.
 PT Humanised immunoglobulin reactive with alpha4-beta7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Claim 15; Fig 12; 145pp; English.
 CC The present sequence represents the light chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal addressin cell adhesion molecule-1 (MadCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MadCAM-1, which is present of high endothelial
 CC venules in muscosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 SQ Sequence 138 AA;

Query Match 87.5%; Score 608; DB 1; Length 138;
 Best Local Similarity 87.1%; Pred. No. 1.2e-42;
 Matches 115; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGGVVYTORPLSPVSGDVSISCRSSOSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGGVVYTORPLSPVSGDVSISCRSSOSLAKSYGNTYLSW 60
 QY 61 YLHAPGSPOLLIIYGISNRFSGVDPDRFSGSGSDFTIKITIKPEDIGMYTCLOGTHOP 120
 DB 61 YLHAPGSPOLLIIYGISNRFSGVDPDRFSGSGSDFTIKITIKPEDIGMYTCLOGTHOP 120
 QY 121 YTFGGGTRLEIK 132
 DB 121 YTFGGGTRLEIK 132

RESULT 4
 W14942
 ID W14942 standard; Protein; 238 AA.
 AC W14942;
 DT 16-JUN-1997 (first entry)
 DE 3F4 Human IgG4 expression plasmid insert product (light chain).
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 OS Mus sp.
 PN W09711971-A1.
 PD 03-APR-1997.
 PR 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR WPI; 97-212855/19.
 DR N-PSDB; T62938.

PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure: Page 65-66; 105pp; English.
 CC Heavy chain (W14941) and light chain (W14942) sequences
 CC correspond to murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 3F4 (see also W14937-38). They
 CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
 CC also T62938). A chimeric antibody specific for porcine VCAM can be
 CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 SQ Sequence 238 AA;

Query Match 80.5%; Score 559.5; DB 1; Length 238;
 Best Local Similarity 81.1%; Pred. No. 1.7e-38;
 Matches 107; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSFQDVVISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSSSDVVMQPLSLPVSLGQASISCRSSQSLVHNSNNTYLQW 59
 QY 61 YLHKPGSPOLLITIGISNRSFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMKYCLOGTQHP 120
 DB 60 YLQKPGSPKLLITKYVNSFSGVDPDRFSGSGGTDFTLKISRVEAEDLGYVFCSTGTHVP 119
 QY 121 YTFGGGTRLEIK 132
 DB 120 YTFGGGTRLEIK 131

RESULT 5
 W14937
 ID W14937 standard; Protein; 238 AA.
 AC W14937;
 DT 16-JUN-1997 (first entry)
 DE Murine anti-porcine VCAM 3F4 light chain.
 KM Xenotransplantation; graft rejection; cell interaction; pig;
 KM vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KM chimeric antibody; diagnosis.
 OS Mus sp.
 FS Key
 FT region Location/Qualifiers
 FT 43..58
 FT /Label= CDR1
 FT 74..80
 FT /Label= CDR2
 FT 113..121
 FT /Label= CDR3
 FT region
 PN MO9711971-A1.
 PD 03-APR-1997.
 PE 27-SEP-1996; U15575.
 PF 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR N-PSDB: T62934
 DR WPI: 97-212855/19.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure: Page 52-53; 105pp; English.
 CC Light chain (W14937) and heavy chain (W14938) sequences are
 CC provided for the murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody (Mab) 3F4. Hybridoma 3F4 was
 CC produced by standard techniques using recombinant, soluble porcine
 CC VCAM as immunogen. Chimeric antibodies can be produced by cloning
 CC Mab 3F4 and 2A2 (see also W14931-32) variable regions into
 CC expression plasmid PAPEX-3P modified to contain the human gamma4
 CC constant region in place of the human gamma1 CI region. Sequences
 CC are provided for 3F4 (chimeric) human G2/G4 CDNA (W14939), a 3F4

CC human G2/G4 expression plasmid insert product (W14940), and 3F4
 CC human IgG4 expression plasmid insert products (W14941-42). The
 CC chimeric antibodies are specific for porcine VCAM. They are useful
 CC for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs
 CC into human recipients.
 SQ Sequence 238 AA;

Query Match 80.5%; Score 559.5; DB 1; Length 238;
 Best Local Similarity 81.1%; Pred. No. 1.7e-38;
 Matches 107; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSFQDVVISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSSSDVVMQPLSLPVSLGQASISCRSSQSLVHNSNNTYLQW 59
 QY 61 YLHKPGSPOLLITIGISNRSFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMKYCLOGTQHP 120
 DB 60 YLQKPGSPKLLITKYVNSFSGVDPDRFSGSGGTDFTLKISRVEAEDLGYVFCSTGTHVP 119
 QY 121 YTFGGGTRLEIK 132
 DB 120 YTFGGGTRLEIK 131

RESULT 6
 W34518
 ID W34518 standard; Protein; 131 AA.
 AC W34518;
 DT 19-MAR-1998 (first entry)
 DE Variable kappa chain of antibody from hybridoma 1-706-139.
 KM Variable region coding sequence; constant region epitope; hybridoma;
 KM antibody detection; antigen/antibody complex; variable heavy chain.
 OS Mus musculus.
 FS Mus 27486-A1.
 PN MO9727486-A1.
 PD 31-JUL-1997.
 PF 17-JAN-1997; U01074.
 PR 23-JAN-1996; US-589939.
 PA (ABBO) ABBOTT LAB.
 PI Golden AM, Hackett JR, Hoff JA, Ostrow DH;
 PI WPI: 97-393833/36.
 DR N-PSDB: T98835.
 PT Use of antibody constant region epitope(s) - as control or
 PT calibrator reagents in assays for detecting the presence of an
 PT antibody in a test sample
 PS Disclosure: Page 62-63; 109pp; English.
 CC This sequence represents the variable kappa chain of the antibody
 CC produced by hybridoma 1-706-139, and can be detected using the method of
 CC the invention. The method is for detecting the presence of antibody which
 CC may be present in a test sample. It comprises contacting a test sample
 CC suspected of containing the antibody with an antigen specific for the
 CC antibody to allow the formation of antigen/antibody complexes, detecting
 CC the presence of the antibody which may be present in the test sample and
 CC employing, as a control or calibrator, a reagent which binds to the
 CC antigen. The improvement to this method over previous methods, comprises
 CC employing, as the control or calibrator, a reagent comprising one or more
 CC antibody constant region epitopes, where the reagent binds to the antigen
 CC and is homogeneous with respect to specificity and affinity. The method
 CC can also be used for detecting the presence of antibodies developed
 CC against more than one antigen. The method is used particularly for the
 CC detection of human antibodies specific for a given antigen, e.g. HIV-1,
 CC hepatitis E virus, rubella virus, etc. Use of the reagents circumvent all
 CC of the problems associated with using an immune sera in the manufacture
 CC of calibrators and positive controls. The present reagents can be readily
 CC and reproducibly generated in virtually unlimited quantities and are also
 CC useful for quantitating, and monitoring the integrity of, the antigen
 CC used in assays.
 SQ Sequence 131 AA;

Query Match 80.4%; Score 558.5; DB 1; Length 131;
 Best Local Similarity 81.1%; Pred. No. 1.1e-38;

Matches 107; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPLVLLVLEWIPVSGDVTOTPLSPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPLVLLVLEWIPVSGDVTOTPLSPVSGDQVSISSCRSSQSLAKSYGNTYLSW 59

QY 61 YLHRPGSPOLLTYGINSRSGVDPDRSGSGGDTFTLKISTIKPELGMYYCLOGTHOP 120
 DB 60 YLQKPGSPOLLTYGINSRSGVDPDRSGSGGDTFTLKISTIKPELGMYYCLOGTHOP 119

QY 121 YTFGGGTRLEIK 132
 DB 120 YTFGGGTRLEIK 131

RESULT 7
 W03199
 ID W03199 standard; Protein; 149 AA.
 AC W03199;
 DT 26-FEB-1997 (first entry)
 DE Anti-Idiotypic monoclonal antibody 1A7 variable light chain.
 KW Murine; mouse; anti-Idiotypic; monoclonal antibody; Mab; 1A7;
 KW variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
 KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
 KW malignant melanoma; soft tissue sarcoma; small cell carcinoma;
 KW vaccine; treatment; palliate; detection; diagnosis;
 KW recombinant production; purification; probe; primer; assay;
 KW amplification; gene therapy.
 OS Mus musculus.

FT Key Location/Qualifiers
 FT peptide 1..19
 FT region /label= sig_peptide
 FT region 20..42
 FT region /note= "framework region 1"
 FT region 43..58
 FT region /note= "complementarity determining region 1"
 FT region 59..73
 FT region /note= "framework region 2"
 FT region 74..80
 FT region /note= "complementarity determining region 2"
 FT region 81..112
 FT region /note= "framework region 3"
 FT region 113..121
 FT region /note= "complementarity determining region 3"
 FT region 122..131
 FT region /note= "framework region 4"

PN W09622373-A2.
 PD 25-JUL-1996.
 PR 17-JAN-1996; U00882.
 PR 17-JAN-1995; US-372676.
 PR 16-JAN-1996; US-372676.
 PA (KENT) UNIV KENTUCKY.
 PI Chatterjee M., Chatterjee SK, Foon KA;
 DR WPI: 96-354530/35.
 DR N-PSDB; T31332.
 FT Monoclonal antibody 1A7 and related polynucleotide(s) and
 FT polypeptide(s) - useful to treat or palliate a GD2-associated
 FT disease, e.g. melanoma and glioma
 PS Claim 8; Fig 1; 141pp; English.

CC The present sequence is that of the murine anti-Idiotypic monoclonal
 CC antibody (Mab) 1A7 variable light chain. Mab 1A7 was raised against
 CC the anti-ganglioside 2 (GD2) Mab 14G2a, which binds an unique
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
 CC of the lung, Mab 1A7, or its cDNA can be used in a vaccine to treat
 CC or palliate such diseases. They can also be used to reduce the
 CC risk of recurrence of a clinically detectable tumour, and detect an
 CC anti-GD2 Ab bound to a tumour cell.
 CC Mab 1A7 overcomes immune tolerance and induces an immune response
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and
 CC GD2-specific cells (cellular response). It can be used to purify
 CC anti-1A7 (Ab3), anti-GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or

CC anti-GD2 in a sample or measure the level of cellular anti-1A7 or
 CC anti-GD2 activity.
 CC The cDNA can be used in expression systems for 1A7 prodn., and in
 CC the prepn. of probes and primers for respectively assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.
 SQ Sequence 149 AA;

Query Match 79.8%; Score 554.5; DB 1; Length 149;
 Best Local Similarity 79.5%; Pred. No. 2,7e-38;
 Matches 105; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 1 MKLPLVLLVLEWIPVSGDVTOTPLSPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPLVLLVLEWIPVSGDVTOTPLSPVSGDQVSISSCRSSQSLAKSYGNTYLSW 59

QY 61 YLHRPGSPOLLTYGINSRSGVDPDRSGSGGDTFTLKISTIKPELGMYYCLOGTHOP 120
 DB 60 YLQKPGSPOLLTYGINSRSGVDPDRSGSGGDTFTLKISTIKPELGMYYCLOGTHOP 119

QY 121 YTFGGGTRLEIK 132
 DB 120 YTFGGGTRLEIK 131

RESULT 8
 R52772
 ID R52772 standard; Protein; 131 AA.
 AC R52772;
 DT 24-JAN-1995 (first entry)
 DE Murine KC-4 immunoglobulin light chain variable region (deduced).
 KW Immunoglobulin variable domain; primer; polymerase chain reaction;
 KW chimeric antibody; human milk fat globule; human breast carcinoma;
 KW murine anti-human carcinoma monoclonal antibody KC-4.
 OS Mus musculus.

FT Key Location/Qualifiers
 FT protein 20..131
 FT region /label= KC-4_mature_VL-chain
 FT region 20..42
 FT region /label= FR1
 FT region 43..58
 FT region /label= CDRI
 FT region 59..73
 FT region /label= FR2
 FT region 74..80
 FT region /label= CDR2
 FT region 81..112
 FT region /label= FR3
 FT modified_site 98..100
 FT region /note= "putative glycosylation site"
 FT region 113..121
 FT region /label= CDR3
 FT region 122..131
 FT region /label= FR4

PN W09411508-A.
 PD 26-MAY-1994.
 PR 15-NOV-1993; U11316.
 PR 13-NOV-1992; US-977706.
 PR 13-NOV-1992; US-977707.
 PR 28-SEP-1993; US-128015.
 PA (CANC-) CANCER RES FUND CONTRA COSTA.
 DR WPI: 94-183509/22.
 DR N-PSDB; Q62763.
 FT Chimeric human-murine polypeptide(s) specific for human mammary
 FT fat globule antigen - for imaging, diagnosing and treating
 FT neoplasia, with less undesirable immunogenic response
 PS Example 27; Page 41; 54pp; English.

CC An initial isolation of cDNAs coding for murine anti-human breast
 CC carcinoma Mab KC-4 was performed using PCR with commercially
 CC available primers (see 062751-062758, available from NOVAGEN).
 CC Subsequent cloning using PCR primers J020, J021, J022 and J024
 CC (see 062759-062762) resulted in the isolation of the mouse Ig
 CC variable domains. The amplified cDNAs were sequenced (062763 and

RESULT 11

R32241 standard; Protein; 131 AA.

AC R32241.

DT 09-JUN-1993 (first entry)

DE Chimeric MAb light chain variable region.

KW Monoclonal; antibody; MAb; light; heavy; chain; variable; region;

KW human/mouse; chimeric; difucosyl; Lewis; blood group; murine; BR55-2;

KW expression vector; IgG1; IgG3; pVg; pVg3; gamma; kappa; constant;

KW pVg1c; pVg3c; PCR; plasmid; host cell; sp2/O-Ag 14; electroporation;

KW antigen; Y-6; B-7-2; binding specificity; erythrocyte; diagnosis;

KW cancer; epithelial; breast; colorectal; ovarian; prostate; pancreatic;

KW gastric; small cell lung; immunotherapy; HIV.

OS Mus musculus.

PH Key

FT region

FT 43..58

FT /label- CDR1

FT /note- "Claim 4"

FT region

FT 74..80

FT /label- CDR2

FT /note- "Claim 4"

FT region

FT 113..121

FT /label- CDR3

FT /note- "Claim 4"

EP-528767-A.

PD 24-FEB-1993.

PD 18-AUG-1992; 810633.

PR 21-AUG-1991; GB-018013.

PR 02-MAR-1992; GB-004514.

PA (SANO) SANDOZ LTD.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

PI Co MS.

PI WPI: 93-060580/08.

DR N-PSDB: Q36529.

PT Human-mouse chimeric monoclonal antibodies - recognise di:fucosyl

PT Lewis blood group antigens Y-6 and B-7-2, useful for treating

PT cancer and HIV infection

PS Claim 3; Page 18; 65pp; English.

CC The sequences given in R32241-42 are the light and heavy chain

CC variable regions respectively from a human/mouse chimeric monoclonal

CC antibody (MAb) which recognises the difucosyl Lewis blood group. The

CC murine MAb BR55-2 was used as a basis for the construction of this

CC chimeric MAb. Separate expression vectors were used to express the

CC chimeric human BR55-2 IgG1 and IgG3 antibody light and heavy chains:

CC pVg for the light chain. pVg for the gamma 1 heavy chain and pVg3 for

CC the gamma 3 heavy chain. The actual expressed chimeric BR55-2 light

CC chain gene and the heavy chain gene consist of two adjacent parts.

CC The kappa/gamma constant regions were built into the vectors pVg

CC and pVg3c (or pVg3c) respectively and the variable regions were

CC constructed by PCR (see also Q36531-33). The resulting plasmids were

CC used to transfect the host cell line sp2/O-Ag 14 by electroporation.

CC The resulting MAb's recognise the difucosyl Lewis blood group antigens

CC Y-6 and B-7-2 but do not induce human anti-mouse antibody response.

CC The MAb's show a restricted binding specificity which is associated

CC with a lack of cross-reactivity to related antigens expressed on

CC blood cells eg. erythrocytes. This allows the MAb's to be particularly

CC useful for therapeutic use in humans. The MAb's are useful in the

CC diagnosis and treatment of cancer of epithelial origin, eg. breast,

CC colorectal, ovarian, prostate, pancreatic or gastric cancer and small

CC cell lung cancer. The MAb's are also useful for immunotherapy of HIV

CC infections since the Lewis Y antigen is also selectively expressed on

CC HIV infected cells.

CC Sequence 131 AA;

SQ

Query Match 78.2%; Score 543.5; DB 1; Length 131;

Best Local Similarity 78.0%; Pred. No. 1.8e-37;

Matches 103; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

OY 1 MKLPVRLVLLLEWIPVSGGVVVTQTPLSPVSGDOVISCRSSQSILAKSGYNTYLSW 60

Db 1 MKLPVRLVLLLEWIPVSGGVVVTQTPLSPVSGDOVISCRSSQSILAKSGYNTYLSW 59

OY 61 YLHRGSPOLLITIGISNRFSGVDPDRSGSGGDTFLTKISTIREPDLGMWYCYCQTHOP 120

Db 60 YLHRGSPKLLISRVSRFSGVDPDRSGSGGDTFLTKISREAEEDLGYVYCFQSGHVP 119

OY 121 YTFGGGTLEIK 132

Db 120 YTFGGGTLEIK 131

RESULT 12

R31587 standard; Protein; 131 AA.

AC R31587.

DT 09-JUN-1993 (first entry)

DE BR55-2 light chain variable domain.

KW Monoclonal; antibody; MAb; light; heavy; chain; variable; region;

KW human/mouse; chimeric; difucosyl; Lewis; blood group; murine; BR55-2;

KW expression vector; IgG1; IgG3; pVg; pVg3; gamma; kappa; constant;

KW pVg1c; pVg3c; PCR; plasmid; host cell; sp2/O-Ag 14; electroporation;

KW antigen; Y-6; B-7-2; binding specificity; erythrocyte; diagnosis;

KW cancer; epithelial; breast; colorectal; ovarian; prostate; pancreatic;

KW gastric; small cell lung; immunotherapy; HIV.

OS Mus musculus.

PH Key

FT peptide

FT 20..131

FT /note- "Mature peptide"

EP-528767-A.

PD 24-FEB-1993.

PD 18-AUG-1992; 810633.

PR 21-AUG-1991; GB-018013.

PR 02-MAR-1992; GB-004514.

PA (SANO) SANDOZ LTD.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

PI Co MS.

PI WPI: 93-060580/08.

DR N-PSDB: Q36536.

PT Human-mouse chimeric monoclonal antibodies - recognise di:fucosyl

PT Lewis blood group antigens Y-6 and B-7-2, useful for treating

PT cancer and HIV infection

PS Disclosure; Fig 8; 65pp; English.

CC The sequences given in R31587-88 represent the light and heavy chain

CC variable regions respectively from the murine monoclonal (MAb) BR55-2.

CC BR55-2 was used as a basis for the construction of a chimeric MAb

CC which recognises the difucosyl Lewis blood group. Separate expression

CC vectors were used to express the chimeric human BR55-2 IgG1 and IgG3

CC antibody light and heavy chains: pVg for the light chain, pVg for the

CC gamma 1 heavy chain and pVg3 for the gamma 3 heavy chain. The actual

CC expressed chimeric BR55-2 light chain gene and the heavy chain gene

CC consist of two adjacent parts. The kappa/gamma constant regions were

CC built into the vectors pVg and pVg3c (or pVg3c) respectively and the

CC variable regions were constructed by PCR. The resulting plasmids were

CC used to transfect the host cell line sp2/O-Ag 14 by electroporation.

CC The resulting MAb's recognise the difucosyl Lewis blood group antigens

CC Y-6 and B-7-2 but do not induce human anti-mouse antibody response.

CC The MAb's show a restricted binding specificity which is associated with

CC a lack of cross-reactivity to related antigens expressed on blood

CC cells eg. erythrocytes. This allows the MAb's to be particularly

CC useful for therapeutic use in humans. The MAb's are useful in the

CC diagnosis and treatment of cancer of epithelial origin, eg. breast,

CC colorectal, ovarian, prostate, pancreatic or gastric cancer and small

CC cell lung cancer. The MAb's are also useful for immunotherapy of HIV

CC infections since the Lewis Y antigen is also selectively expressed on

CC HIV infected cells.

CC Sequence 131 AA;

SQ

Query Match 78.2%; Score 543.5; DB 1; Length 131;

Best Local Similarity 78.0%; Pred. No. 1.8e-37;

Matches 103; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

```

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSPFGDQVSISSCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSPFGDQVSISSCRSSQSLAKSYGNTYLSW 59
QY 61 YLHKPQSPQLLYGSIISNRFSGVDPDRFSSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 120
DB 60 YLHKPQSPQLLYGSIISNRFSGVDPDRFSSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 119
QY 121 YTFGGGSKLEIK 132
DB 120 YTFGGGSKLEIK 131

RESULT 13
R32245
ID R32245 standard; Protein: 131 AA.
AC R32245;
DT 09-JUN-1993 (first entry)
DE BR55-2 murine IgG3 light chain variable domain.
KW Monoclonal; antibody; MAb; light; heavy; chain; variable; region;
KW human/mouse; chimeric; difucosyl; Lewis; blood group; murine; BR55-2;
KW expression vector; IgG1; IgG3; pVc; pVg3; pVg3; gamma; kappa; constant;
KW pVg1c; pVg3c; PCR; plasmid; host cell; sp2/O-Ag 14; electroporation;
KW antigen; Y 6; B-7-2; binding specificity; erythrocyte; diagnosis;
KW cancer; epithelial; breast; colorectal; ovarian; prostate; pancreatic;
KW gastric; small cell lung; immunotherapy; HIV.
OS Mus musculus.
FH Key
FT protein
FT location/Qualifiers
FT 20..131
FT /note="Mature protein"
FT region
FT 43..58
FT /label= CDR1
FT region
FT 74..80
FT /label= CDR2
FT region
FT 113..121
FT /label= CDR3

EP-528767-A.
PD 24-FEB-1993.
PF 18-AUG-1992; 810633.
PR 21-AUG-1991; GB-018013.
PR 02-MAR-1992; GB-004514.
PA (SANO ) SANDOZ LTD.
PA (SANO ) SANDOZ PATENT GMBH.
PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Co MS, Iolbner H;
PI WPI: 93-060580/08.
DR N-PSDB; Q36534.
PT Human-mouse chimeric monoclonal antibodies - recognise difucosyl
PT Lewis blood group antigens Y-6 and B-7-2, useful for treating
PT cancer and HIV infection
PS Disclosure: Fig 3: 65pp; English.
CC The sequences given in R32245-46 represent the light and heavy chain
CC variable regions respectively from the murine monoclonal (MAb) BR55-2
CC IgG3. BR55-2 was used as a basis for the construction of a chimeric
CC MAb which recognises the difucosyl Lewis blood group. Separate
CC expression vectors were used to express the chimeric human BR55-2 IgG1
CC and IgG3 antibody light and heavy chains: pVc for the light chain, pVg
CC for the gamma 1 heavy chain and pVg3 for the gamma 3 heavy chain. The
CC actual expressed chimeric BR55-2 light chain gene and the heavy chain
CC gene consist of two adjacent parts. The kappa/gamma constant regions
CC were built into the vectors pVc and pVg1c (or pVg3c) respectively and
CC the variable regions were constructed by PCR. The resulting plasmids
CC were used to transfect the host cell line sp2/O-Ag 14 by electro-
CC poration. The resulting Mabs recognise the difucosyl Lewis blood
CC group antigens Y-6 and B-7-2 but do not induce human anti-mouse anti-
CC body response. The Mabs show a restricted binding specificity which is
CC associated with a lack of cross-reactivity to related antigens
CC expressed on blood cells eg. erythrocytes. This allows the Mabs to be
CC particularly useful for therapeutic use in humans. The Mabs are
CC useful in the diagnosis and treatment of cancer of epithelial origin,
CC eg. breast, colorectal, ovarian, prostate, pancreatic or gastric
CC cancer and small cell lung cancer. The Mabs are also useful for

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CC Immunotherapy of HIV infections since the Lewis Y antigen is also
CC selectively expressed on HIV infected cells.
SQ Sequence 131 AA;

Query Match 77.3%; Score 537.5; DB 1; Length 131;
Best Local Similarity 77.3%; Pred. No. 5, 6e-37;
Matches 102; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

```

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSPFGDQVSISSCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSPFGDQVSISSCRSSQSLAKSYGNTYLSW 59
QY 61 YLHKPQSPQLLYGSIISNRFSGVDPDRFSSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 120
DB 60 YLHKPQSPQLLYGSIISNRFSGVDPDRFSSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 119
QY 121 YTFGGGSKLEIK 132
DB 120 YTFGGGSKLEIK 131

RESULT 14
R52822
ID R52822 standard; Protein: 131 AA.
AC R52822;
DT 25-JAN-1995 (first entry)
DE Humanised murine KC-4 immunoglobulin light chain V-region.
KW Immunoglobulin variable domain; primer; polymerase chain reaction;
KW chimeric antibody; human mammary fat globule; human breast carcinoma;
KW murine anti-HMFg monoclonal antibody KC-4; humanised analogue.
OS Chimeric Mus musculus.
PN MO9411509-A.
PD 26-MAR-1994.
PF 16-NOV-1993; U11445.
PR 16-NOV-1992; US-977696.
PR 30-SEP-1993; US-129930.
PR 08-OCT-1993; US-134346.
PA (CANC-) CANCER RES FUND CONTRA COSTA.
PI Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;
PI WPI: 94-183510/22.
DR N-PSDB; Q62803.
PT New analogue peptide(s) comprising antibody variable regions -
PT used to develop prods. for use in the detection, diagnosis,
PT therapy and prevention of neoplasms
PS Example 75: Page 95; 109pp; English.
CC This sequence represents a humanised murine anti-human carcinoma
CC KC-4 antibody light chain variable region. The humanised antibody is
CC useful for carcinoma therapy and diagnosis and for in vivo imaging
CC of neoplastic cells. It is also of use in inhibiting the growth of
CC a primary or metastasised neoplasm.
SQ Sequence 131 AA;

```

Query Match 77.3%; Score 537.5; DB 1; Length 131;
Best Local Similarity 77.3%; Pred. No. 5, 6e-37;
Matches 102; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

```

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSPFGDQVSISSCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSPFGDQVSISSCRSSQSLAKSYGNTYLSW 59
QY 61 YLHKPQSPQLLYGSIISNRFSGVDPDRFSSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 120
DB 60 YLHKPQSPQLLYGSIISNRFSGVDPDRFSSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 119
QY 121 YTFGGGSKLEIK 132
DB 120 YTFGGGSKLEIK 131

RESULT 15

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R70470
 ID R70470 standard; Protein; 131 AA.
 AC R70470;
 DT 27-OCT-1995 (first entry)
 DE Humanised anti-KC-4 antibody VL FR-H2.
 KW Anti-KC-4 antibody; humanised antibody; cancer.
 OS Synthetic.
 PN WO9510776-A.
 PD 20-APR-1995.
 PE 16-NOV-1993; U11444.
 PR 08-OCT-1993; US-134346.
 PA (CANC-) CANCER RESEARCH FUND CONTRA COSTA.
 PI Ceriani RL, Docuto JJR, Peterson JA;
 DR WPI; 95-161912/21.
 DR N-PSDB; Q87533.
 PT New humanised anti-KC-4 monoclonal antibody - used for detection of
 PT cancer cells. In vivo imaging, ex-vivo purging and treatment of
 PT cancers
 PS Claim 2; Table 24, page 51; 61pp; English.
 CC Hybridomas were prep'd. based on the anti-KC-4 mouse hybridoma ATCC
 CC HB 8710 (US4708930). The murine variable regions were modified at
 CC particular AAs by PCR to provide humanised sequences. The anti-KC-4
 CC humanised DNA sequences for the VH and VL segments are shown in
 CC Q87533 and Q87533 respectively. Plasmid constructions comprising
 CC the humanised variable regions and the human constant regions were
 CC then used to transfrom SP2/0-Ag14 myeloma cells to produce the
 CC humanised anti-KC-4 Mabs. The deduced AA sequences of the
 CC humanised anti-KC-4 variable light and heavy chains are given in
 CC R70470 and R70471 respectively.
 SQ Sequence 131 AA;

Query Match 77.3%; Score 537.5; DB 1; Length 131;
 Best Local Similarity 77.3%; Pred. No. 5.6e-37;
 Matches 102; Conservative 12; Mismatches 17; Indels 1; Gaps 1;
 QY 1 MKLEPVRLVLLFVPIVSGGVVYVQTPLSLPVFSGDOVISICRSQSGLAKSYGNTYLSW 60
 Db 1 MKLEPVRLV-LMFVPIPASSSDVLTMTOTPLSLPVPGEPASISCRSSQSIHNSNGNTYLEW 59
 QY 61 YLHPPGSPOLLITIGISNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYTCLOGTHOP 120
 Db 60 YLQPPGSPOLLITIKVSIRESGVDPDRFSGSGGTDFTLKISRVEAEDVGYTCFQGSHP 119
 QY 121 YTFGGTKLEIK 132
 Db 120 YTFGGTKLEIK 131

Search completed: May 11, 1999, 12:14:53
 Job time: 2100 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 12:00:26 ; Search time 962.98 Seconds
(Without alignments)
1560.334 Million cell updates/sec

Title: US-08-700-737-14

Perfect score: 420
Sequence: 1 ATGGATGAGAGCTGTATCAT.....CCTCAGTCACCGTCTCTCA 420

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_in: *
4: gb_om: *
5: gb_om: *
6: gb_pat: *
7: gb_ph: *
8: gb_ph: *
9: gb_ph: *
10: gb_ph: *
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37: gb_ph: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description

1	335.8	80.0	1572	6	A44967	A44967 Sequence 23
2	335.8	80.0	1572	6	I64458	I64458 Sequence 23
3	335.2	79.8	446	13	S71019	S71019 IgG1-anti-e
4	333.6	79.4	417	13	AF045500	AF045500 Mus muscu
5	332.4	79.1	462	13	M0835	M0835 Mouse IgM
6	330.4	78.7	417	13	M0835	M0835 Mouse IgM
7	328.8	78.3	417	13	AF045487	AF045487 Mus muscu
8	328.8	78.3	429	13	M0835	M0835 Mouse IgM
9	327.2	77.9	429	6	I33384	I33384 Sequence 6
10	322.4	76.8	418	13	M0835	M0835 Mouse IgM
11	319.2	76.0	420	13	AF045499	AF045499 Mus muscu
12	317.2	75.5	1069	13	M0835	M0835 Mouse IgM
13	314.4	74.9	501	6	A27941	A27941 Coding regi
14	314.4	74.9	501	6	I26277	I26277 Sequence 23
15	312.8	74.5	471	13	M0835	M0835 Mouse IgM
16	309.6	73.7	454	13	M0835	M0835 Mouse IgM
17	309.4	73.7	423	13	M0835	M0835 Mouse IgM
18	307	73.1	411	13	M0835	M0835 Mouse IgM
19	306.6	73.0	411	13	M0835	M0835 Mouse IgM
20	306.4	73.0	411	13	M0835	M0835 Mouse IgM
21	306.4	73.0	1544	13	M0835	M0835 Mouse IgM
22	305.6	72.8	923	13	M0835	M0835 Mouse IgM
23	304.6	72.5	408	13	AF045489	AF045489 Mus muscu
24	303.2	72.2	469	13	M0835	M0835 Mouse IgM
25	302.2	72.0	451	13	M0835	M0835 Mouse IgM
26	302	71.9	1068	13	M0835	M0835 Mouse IgM
27	301.4	71.8	351	6	I33386	I33386 Sequence 10
28	300.8	71.6	411	13	M0835	M0835 Mouse IgM
29	299.6	71.3	566	15	SYNCHIC1	SYNCHIC1
30	299.2	71.2	424	13	M0835	M0835 Mouse IgM
31	299	71.2	363	13	MMY20292B	MMY20292B
32	298.8	71.1	1068	13	M0835	M0835 Mouse IgM
33	298.4	71.0	426	13	M0835	M0835 Mouse IgM
34	298.2	71.0	504	13	M0835	M0835 Mouse IgM
35	298	71.0	444	13	M0835	M0835 Mouse IgM
36	297.6	70.9	426	13	M0835	M0835 Mouse IgM
37	297.4	70.8	363	13	MM37F2A	MM37F2A
38	297.2	70.8	1068	13	M0835	M0835 Mouse IgM
39	296.2	70.5	358	13	MMND54C	MMND54C
40	295	70.2	408	13	M0835	M0835 Mouse IgM
41	294.8	70.2	523	13	M0835	M0835 Mouse IgM
42	294.6	70.1	357	13	AF012069	AF012069 Mus muscu
43	294	70.0	474	13	MMND10C	MMND10C
44	294	70.0	367	13	MMND10C	MMND10C
45	293.6	69.9	357	6	A46580	A46580 Sequence 11

ALIGNMENTS

RESULT 1
LOCUS A44967 1572 bp DNA
DEFINITION Sequence 23 from Patent W09515382.
ACCESSION A44967
NID g2299553
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1572)
AUTHORS Rose, M.S., Boot, C., Copley, C.G., Paterson, D.S., Hall, S.M.,
TITLE Wright, A.F. and Blakey, D.C. DIRECTED AGAINST THE CA55.1 ANTIGEN
JOURNAL BINDING STRUCTURES DIRECTED AGAINST THE CA55.1 ANTIGEN
ZEMECKA LTD (GB)
COMMENT Other publication GB 2297751 960814
Other publication CA 2174972 950605
Other publication ZA 9409266 950605
Other publication AU 1113095 950619.
Location/Qualifiers
1..1572
/organism="unclassified"

FEATURES

source

BASE COUNT 401 a 465 c 378 g 328 t
 ORIGIN

Query Match 80.0%; Score 335.8; DB 6; Length 1572;
 Best Local Similarity 87.6%; Pred. No. 2.1e-95;
 Matches 367; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

1 ATGGGATGGAGCTGATATCATCTCTTCTTGATATCAACAGCTCAAGTCCACCTCCAG 60
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 49 ATGGGATGGAGCTGATATCATCTCTTCTTGATATCAACAGCTCAAGTCCACCTCCAG 108
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 121 TGCAGAGGTTATGCTTACACCTTCAACAGCTGAGTGGTGAAGCAGAGGCT 180
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 229 GGACAAGGCTTCTGAGTGGAGAGATGATCCTTCTGAGATGATATCACTACAT 288
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 289 GAGAAGTTCAAGACAGCAGCAGCAGCAGTACAGCAATCTCCACAGCAGCTACATG 348
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 301 CAGCTCAGCAGCCTGACATCTGAGAGCTGCTGCTACTATTTGCAAGAGGGGTTAC 360
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 349 CAACTCAGCAGCCTGACATCTGAGAGCTGCTGCTACTATTTGCAAGAGGGGCTC 408
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 361 GAGGATGGAGCTATGCTTCTGACTAGTGGGTCAGAGCAGCAGCTCCCTCC 419
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 409 TATGTTACGACAGCTATGAGTACTGAGGCTCAAGAGCAGCTCCCTCC 467
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RESULT 2
 LOCUS 164458 1572 bp DNA PAT 26-SEP-1997
 DEFINITION Sequence 23 from patent US 5665357.
 ACCESSION 164458
 NID 92481352
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1572)
 AUTHORS Rose, M. Samuel, Boot, C., Copley, C. Graham, Paterson, D. Stephen,
 Hall, S. Margaret, Wright, A. Firman and Blakey, D. Charles.
 TITLE Antibodies recognizing tumor associated antigen CA 55.1
 JOURNAL Patent: US 5665357-A 23 09-SEP-1997;
 FEATURES
 source Location/Qualifiers
 1..1572 /organism="unknown"
 BASE COUNT 401 a 465 c 378 g 328 t
 ORIGIN

Query Match 80.0%; Score 335.8; DB 6; Length 1572;
 Best Local Similarity 87.6%; Pred. No. 2.1e-95;
 Matches 367; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

1 ATGGGATGGAGCTGATATCATCTCTTCTTGATATCAACAGCTCAAGTCCACCTCCAG 60
 |||||
 49 ATGGGATGGAGCTGATATCATCTCTTCTTGATATCAACAGCTCAAGTCCACCTCCAG 108
 |||||
 61 GTCCACTGCAGCAGCCTGGGCTGAGCTTGAAGCCTGGGACTTCACTGAGAGCTGCC 120
 |||||
 109 GTCCACTGCAGCAGCCTGGGCTGAGCTTGAAGCCTGGGACTTCACTGAGAGCTGCC 168
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 121 TGCAGAGGTTATGCTTACACCTTCAACAGCTGAGTGGTGAAGCAGAGGCT 180
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|||||
 169 TGCAGAGGCTTCTGAGTGGAGAGATGATCCTTCTGAGATGATATCACTACAT 228
 |||||
 181 GGACAAGGCTTCTGAGTGGAGAGATGATCCTTCTGAGATGATATCACTACAT 240
 |||||
 229 GGACAAGGCTTCTGAGTGGAGAGATGATCCTTCTGAGATGATATCACTACAT 288
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 241 CAAAATTCAGAGCAGCAGCATTGACTAGACATTTCTCCAGCAGCAGCTACATG 300
 |||||
 289 GAGAAGTTCAAGACAGCAGCAGCAGCAGTACAGCAATCTCCACAGCAGCTACATG 348
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 301 CAGCTCAGCAGCCTGACATCTGAGAGCTGCTGCTACTATTTGCAAGAGGGGTTAC 360
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 361 GAGGATGGAGCTATGCTTCTGACTAGTGGGTCAGAGCAGCAGCTCCCTCC 419
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 409 TATGTTACGACAGCTATGAGTACTGAGGCTCAAGAGCAGCTCCCTCC 467
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RESULT 3
 LOCUS 571019 446 bp mRNA ROD 22-SEP-1994
 DEFINITION IgG1-erbB-2 product monoclonal antibody heavy chain variable
 region [mice, E401 hybridoma, mRNA partial, 446 nt].
 ACCESSION 571019
 NID 9546187
 KEYWORDS
 SOURCE Mus sp. E401 hybridoma.
 ORGANISM Mus sp.
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Mus.

REFERENCE 1 (bases 1 to 446)
 AUTHORS Ishida, T., Tsujisaki, M., Hinoda, Y., Imai, K. and Yachi, A.
 TITLE Establishment and characterization of mouse-human chimeric
 monoclonal antibody to erbB-2 product
 Jpn. J. Cancer Res. 85 (2), 172-178 (1994)
 JOURNAL 94193471
 MEDLINE
 REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI glibseq 149475] from the original journal article.
 This sequence comes from Fig. 2.
 FEATURES
 source Location/Qualifiers
 1..446 /organism="Mus sp."
 /db_xref="taxon:10095"
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 variable region"
 /gene="IgG1"
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 /gene="IgG1"
 /note="This sequence comes from Fig. 2. Protein sequence
 is in conflict with the conceptual translation;
 mismatches (11f->T), 63(0->G)"]
 /codon_start=1
 /product="anti-erbB-2 product monoclonal antibody heavy
 chain variable region"
 /db_xref="PDB:9546188"
 /translation="IDMGSMIFLFAVATADVHSQVLOQPGAEIVKPEASVLSCK
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 QLSLTSEDSAVVYCAETVDEYEDDYDGOGTTLVSSGSKIPV"

BASE COUNT 114 a 117 c 117 g 98 t
 ORIGIN

Query Match 79.8%; Score 335.2; DB 13; Length 446;
 Best Local Similarity 87.4%; Pred. No. 2.8e-95;
 Matches 367; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

1 ATGGGATGGAGCTGATATCATCTCTTCTTGATATCAACAGCTCAAGTCCACCTCCAG 60

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/db_xref="taxon:10090"
/cell_line="spleen cell hybridoma"
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/db_xref="PID:92906084"
/translation="MGWSCIILVSTATGVHSGVOLQPGAEILVRPTSYLKCKAS
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SLTSEDSAVHYVCARGQLPGRGFAVMQGRILTVSA"
58..351
/gene="Igh"
352..384
/gene="Igh"
385..>417

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/db_xref="PID:g196946"
 /translation="MGMSCTILFLVAATGVHSOVLQOPGAEIVKPGASVLSCKAS
 GYFTSYNHWKORRGLEIMIGRIDPSSGKTKNEKSKATLTVDRSSSTAVMOL
 SLLTSDSAVYVCARDYGVSSYFDWGGTILTVSS"
 mat_peptide /note="Ig heavy chain"
 50..>462

BASE COUNT 118 a 120 c 112 g 112 t
 ORIGIN Chromosome 12.

Query Match 79.1%; Score 332.4; DB 13; Length 462;
 Best Local Similarity 88.8%; Pred. No. 2.1e-94;
 Matches 373; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 1 ATGGAGTGGAGCTGTATCATCTCTCTTGTGTATCAACAGCTAGTGTCTCATCCAG 60
 Db 49 ATGGAGTGGAGCTGTATCATCTCTTGTGTATCAACAGCTAGTGTCTCATCCAG 108
 QY 61 GTCCACTGCAGCAGCTGGGGCTGAGCTGTGTGAAGCTGGGACTGAGTGAAGCTGTC 120
 Db 109 GTCCACTGCAGCAGCTGGGGCTGAGCTGTGTGAAGCTGGGACTGAGTGAAGCTGTC 168
 QY 121 TGCAGGGTATGCTGATCCTTACCTGACAGCTAGTGCATGCTGGTGAAGCAGAGCT 180
 Db 169 TGCAGGGTATGCTGATCCTTACCTGACAGCTAGTGCATGCTGGTGAAGCAGAGCT 228
 QY 181 GGACAAAGCCTTGTAGTGTGAGAGATGATGATCTCTGTAGATTAATTAATTAATTAAT 240
 Db 229 GGACAAAGCCTTGTAGTGTGAGAGATGATGATCTCTGTAGATTAATTAATTAATTAAT 288
 QY 241 CAAATATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 Db 289 GAGAAAGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 348
 QY 301 CAGCTGAGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 349 CAGCTGAGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 408
 QY 361 GAGGATGAGGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 408 -----TAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 462

RESULT 6
 MUSIGHBX 417 bp mRNA ROD 03-MAY-1985
 LOCUS Mouse Ig active H-chain, C57BL/6 b-NP response from Bl-8, VH-II
 DEFINITION -mRNA.
 ACCESSION J00529
 NID 9195114
 KEYWORDS C-region; V-region; Immunoglobulin heavy chain; variable region
 SOURCE subgroup VH-II.
 ORGANISM Mus musculus
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Euthera; Rodentia; Sciurognathi; Myomorphia; Muridae;
 Murinae; Mus.
 1 (bases 1 to 417)
 Bothwell, A.L.M., Paskind, M., Reth, M., Imanishi-Kari, T., Rejzsky, K.
 and Baltimore, D.
 Heavy chain variable region contribution to the b-NP family of
 antibodies: Somatic mutation evident in a gamma-2a variable region
 Cell 24, 625-637 (1981)
 81234548

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 COMMENT
 [1] characterized the C57BL/6 response to NP proteins, termed the
 b-NP response because this mouse strain carries the b-19H
 haplotype.
 Three hybridoma clones were sequenced, two from b-NP hybridomas
 B1-8 and S43 and one from MOPC21 to show the differences between
 b-NP and non-b-NP genes. Seven b-NP-homologous germline genes were
 selected to determine which may be responsible for the b-NP
 response. VH-186-2 seems to be the gene coding for that response
 and is called the b-NP gene. The others are termed b-NP-related

because of their homology with 186-2.
 The BALB/c NP protein response (a-NP, a-19H haplotype) is reported
 in separate entries.
 Location/Qualifiers

FEATURES
 source 1..417
 /organism="Mus musculus"
 /db_xref="taxon:10090"

sig_peptide 1..57
 /note="Ig H-chain V-region from Bl-8 signal peptide"

CDS 1..>417
 /note="Ig H-chain V-region from Bl-8"

mat_peptide /db_xref="PID:g195115"
 /translation="MGMSCTILFLVAATGVHSOVLQOPGAEIVKPGASVLSCKAS
 GYFTSYNHWKORRGLEIMIGRIDPSSGKTKNEKSKATLTVDRSSSTAVMOL
 SLLTSDSAVYVCARDYGVSSYFDWGGTILTVSS"
 58..>417
 /note="Ig H-chain V-region from Bl-8 mature peptide"

BASE COUNT 102 a 107 c 113 g 95 t
 ORIGIN 71 bp upstream of PstI site, chromosome 12.

Query Match 78.7%; Score 330.4; DB 13; Length 417;
 Best Local Similarity 88.3%; Pred. No. 9e-94;
 Matches 371; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 1 ATGGAGTGGAGCTGTATCATCTCTCTTGTGTATCAACAGCTAGTGTCTCATCCAG 60
 Db 1 ATGGAGTGGAGCTGTATCATCTCTCTTGTGTATCAACAGCTAGTGTCTCATCCAG 60
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 Db 61 GTCCACTGCAGCAGCTGGGGCTGAGCTGTGTGAAGCTGGGACTGAGTGAAGCTGTC 120
 QY 121 TGCAGGGTATGCTGATCCTTACCTGACAGCTAGTGCATGCTGGTGAAGCAGAGCT 180
 Db 121 TGCAGGGTATGCTGATCCTTACCTGACAGCTAGTGCATGCTGGTGAAGCAGAGCT 180
 QY 181 GGACAAAGCCTTGTAGTGTGAGAGATGATGATCTCTGTAGATTAATTAATTAATTAAT 240
 Db 181 GGACAAAGCCTTGTAGTGTGAGAGATGATGATCTCTGTAGATTAATTAATTAATTAAT 240
 QY 241 CAAATATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 Db 241 GAGAAAGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 QY 301 CAGCTGAGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 301 CAGCTGAGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 361 GAGGATGAGGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 TAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417

RESULT 7
 AF045487 417 bp mRNA ROD 28-FEB-1998
 LOCUS Mus musculus dc4 anti-poly(dc) monoclonal antibody heavy chain
 DEFINITION variable region, (Igh) mRNA, partial cds.
 ACCESSION AF045487
 NID 92906057
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Euthera;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 417)
 O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
 Anti-DNA antibodies of normal mice immunized with poly(dc) are
 structurally similar to natural autoantibodies
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 417)

AUTHORS O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
 TITLE Direct Submission
 JOURNAL Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA

FEATURES
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 1.417
 /organism="Mus musculus"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /cell_line="spleen cell hybridoma"
 /chromosome="12"

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 /gene="IGH"
 1..>417
 /gene="IGH"

CDS
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 /translation="MGMSYILFLVATGVSQVLOQPGALVPGASVRLSKAS
 GYFTSYVMHMKORPGGLEWIGLHPNNGSTNNEKFTSKATLTVDKSSSTAYVQF
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sig_peptide
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 58..351
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 D_segment
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 BASE COUNT
 ORIGIN

Query Match 78.3%; Score 328.8; DB 13; Length 417;
 Best Local Similarity 88.1%; Pred. No. 2.9e-93;
 Matches 370; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 1 ATGGGATGAGCTGTATCATCTCTTCTTGATCAACAGCTACAGTGTCCACTCCAG 60
 DB 1 ATGGGATGAGCTATATCATCTCTTCTTGATCAACAGCTACAGTGTCCACTCCAG 60
 QY 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTGTGTGAAGCCTGGGACTGAGAAAGCTGCC 120
 DB 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTGTGTGAAGCCTGGGACTGAGAAAGCTGCC 120
 QY 121 TGCAGGGTTATGCTACCTTACCTTACCAAGCTACAGTGTGGTGAAGAGAGGCTT 180
 DB 121 TGCAGGGCTTCTGGCTACCTTACCTTACCAAGCTACAGTGTGGTGAAGAGAGGCTT 180
 QY 181 GGACAAGGCTTGTAGTGGATCGAGAGTATGATCTCTGAGAGTAATTAATACTAAT 240
 DB 181 GGACAAGGCTTGTAGTGGATCGAGAGTATGATCTCTGAGAGTAATTAATACTAAT 240
 QY 241 CAAAAATTCAGAGGAGGAGCCATTGCTAGTACATTTCTCCACAGCAGCTACATG 300
 DB 241 GAGAAAGTTCAGAGGAGGAGCCATTGCTAGTACATTTCTCCACAGCAGCTACATG 300
 QY 301 CAGCTCAGAGCCTGATGATGAGAGTGTGGGCTCTACTATTGTGCAAGAGGGGTTAC 360
 DB 301 CAGCTCAGAGCCTGATGATGAGAGTGTGGGCTCTACTATTGTGCAAGAGGGGTTAC 360
 QY 361 GAGGATGGAGCTATGCTATGACTACTGGGGTCAAGAGCAGCTCAGTACCGTCTCTCA 420
 DB 361 GAGGATGGAGCTATGCTATGACTACTGGGGTCAAGAGCAGCTCAGTACCGTCTCTCA 420

RESULT 8
 LOCUS MUSIVDJA 429 bp mRNA ROD 25-MAY-1995
 DEFINITION Mus musculus germline immunoglobulin heavy chain variable region,
 diversity region, and joining region, 5' end.
 ACCESSION U35315

NID 9829187
 KEYWORDS diversity region; germline; immunoglobulin heavy chain; joining
 region; variable region.
 SOURCE Mus musculus (strain SJL/J) hyperimmunized spleen mRNA.
 ORGANISM Mus musculus

REFERENCE
 1 (bases 1 to 429)
 MILLER P.J. and RODRIGUEZ M.
 A monoclonal autoantibody that promotes central nervous system
 remyelination in a model of multiple sclerosis is a natural
 autoantibody encoded by germline immunoglobulin genes
 J. Immunol. 154 (5), 2460-2469 (1995)

JOURNAL
 MEDLINE
 COMMENT
 On May 24, 1995 this sequence version replaced gi:529401.
 FEATURES
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 /organism="Mus musculus"
 /strain="SJL/J"
 /db_xref="taxon:10090"
 /cell_line="SCH94.03"
 /cell_type="hybridoma"
 /tissue_type="hyperimmunized spleen"
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 SLTSDSAVYVVRGNLYYAMDYMGQSTVTVSS"

sig_peptide
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 /gene="IGH"
 58..420
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 CDS
 1..>429
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 /note="putative"
 /codon_start=1
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 /db_xref="PID:g829188"
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mat_peptide
 58..420
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 /product="immunoglobulin heavy chain"
 BASE COUNT 108 a 111 c 114 g 96 t
 ORIGIN

Query Match 78.3%; Score 328.8; DB 13; Length 429;
 Best Local Similarity 86.4%; Pred. No. 2.9e-93;
 Matches 363; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 ATGGGATGAGCTGTATCATCTCTTCTTGATCAACAGCTACAGTGTCCACTCCAG 60
 DB 1 ATGGGATGAGCTGTATCATCTCTTCTTGATCAACAGCTACAGTGTCCACTCCAG 60
 QY 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTGTGTGAAGCCTGGGACTGAGAAAGCTGCC 120
 DB 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTGTGTGAAGCCTGGGACTGAGAAAGCTGCC 120
 QY 121 TGCAGGGTTATGCTACCTTACCTTACCAAGCTACAGTGTGGTGAAGAGAGGCTT 180
 DB 121 TGCAGGGCTTCTGGCTACCTTACCTTACCAAGCTACAGTGTGGTGAAGAGAGGCTT 180
 QY 181 GGACAAGGCTTGTAGTGGATCGAGAGTATGATCTCTGAGAGTAATTAATACTAAT 240
 DB 181 GGACAAGGCTTGTAGTGGATCGAGAGTATGATCTCTGAGAGTAATTAATACTAAT 240
 QY 241 CAAAAATTCAGAGGAGGAGCCATTGCTAGTACATTTCTCCACAGCAGCTACATG 300
 DB 241 GAGAAAGTTCAGAGGAGGAGCCATTGCTAGTACATTTCTCCACAGCAGCTACATG 300
 QY 301 CAGCTCAGAGCCTGATGATGAGAGTGTGGGCTCTACTATTGTGCAAGAGGGGTTAC 360
 DB 301 CAGCTCAGAGCCTGATGATGAGAGTGTGGGCTCTACTATTGTGCAAGAGGGGTTAC 360
 QY 361 GAGGATGGAGCTATGCTATGACTACTGGGGTCAAGAGCAGCTCAGTACCGTCTCTCA 420
 DB 361 TACTACGGTAGAGCAATTTGACTACTGGGGCAAGGAGCAGCTCAGTACCGTCTCTCA 420

RESULT 9
 LOCUS 13384 429 bp DNA PAT 22-JAN-1997
 DEFINITION Sequence 6 from patent US 5591629.
 ACCESSION 13384
 NID 91824175
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 429)
 AUTHORS Rodriguez, M. and Miller, D.J.
 TITLE Monoclonal antibodies which promote central nervous system remyelination
 JOURNAL Patent: US 5591629-A 6 07-JAN-1997;
 FEATURES
 source location/qualifiers
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 /organism="unknown"
 BASE COUNT 109 a 111 c 113 g 96 t
 ORIGIN

Query Match 77.98; Score 327.2; DB 6; Length 429;
 Best Local Similarity 86.28; Pred. No. 9.2e-93;
 Matches 362; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 ATGGGATGAGCTGTATCATCTCTCTTGGTATCAACAGCTACAGTCCACGCCAG 60
 Db 1 ATGGGATGAGCTGTATCATCTCTCTTGGTATGAGAGCTACAGTGTCTCCAG 60
 QY 61 GTCCACTGACGACGCTGGGCTGAGCTGTGAAGCTGGAGCTCAGTGAAGCTGCC 120
 Db 61 GTCCACTGACGACGCTGGGCTGAGCTGTGAAGCTGGAGCTCAGTGAAGCTGCC 120
 QY 121 TGCAGAGGTTATGGCTACACTTTCACCGCTACTGAGTGCATGGGTAAAGAGGCT 180
 Db 121 TGCAGAGGTTATGGCTACACTTTCACCGCTACTGAGTGCATGGGTAAAGAGGCT 180
 QY 181 GGACAGAGCTTGTAGTGTGAGAGATGATTCCTTGAGATTAATTAATTAATTAAT 240
 Db 181 GGACAGAGCTTGTAGTGTGAGAGATGATTCCTTGAGATTAATTAATTAATTAAT 240
 QY 241 CAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
 Db 241 CAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
 QY 301 CAGCTCAGACCTGATGATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 360
 Db 301 CAGCTCAGACCTGATGATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 360
 QY 361 GAGCAGTGGAGTGTGATGATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 420
 Db 361 GAGCAGTGGAGTGTGATGATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 420

RESULT 10
 MMU01972 418 bp mRNA ROD 30-SEP-1993
 DEFINITION Mus musculus Balb/c anti-CD18 Ig heavy chain variable region mRNA.

ACCESSION MMU01972
 NID 5403069
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 418)
 AUTHORS Hsiao, K., Bajorath, J. and Harris, L.J.
 TITLE Humanization of 60.3, an anti-CD18 antibody
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 418)
 AUTHORS Harris, L.J.
 TITLE Direct Submission
 JOURNAL Submitted (21-SEP-1993) Linda J. Harris, Molecular Immunology,
 Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First
 Avenue, Seattle, WA 98121 USA
 FEATURES
 source location/qualifiers
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 /strain="Balb/c"
 /db_xref="taxon:10090"
 /map="12q32"
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 /tissue_type="spleen"
 /dev_stage="adult"
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 /note="nucleotides 1-25 derived from PCR primer and may not reflect mRNA"
 1..417
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 /db_xref="PID:9403070"
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sig-peptide
 CDS
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exon
 /number=1
 /product="partial signal peptide"
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 /product="carboxyl end of signal peptide and mature heavy chain"
 58..132
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 58..417
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 211..225
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 352..381
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 382..417
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 BASE COUNT 98 a 118 c 110 g 92 t
 ORIGIN

Query Match 76.88; Score 322.4; DB 13; Length 418;
 Best Local Similarity 87.18; Pred. No. 3e-91;
 Matches 366; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 1 ATGGGATGAGCTGTATCATCTCTCTTGGTATCAACAGCTACAGTGTCCAG 60
 Db 1 ATGGGATGAGCTGTATCATCTCTCTTGGTATCAACAGCTACAGTGTCCAG 60
 QY 61 GTCCACTGACGACGCTGGGCTGAGCTGTGAAGCTGGAGCTCAGTGAAGCTGCC 120
 Db 61 GTCCACTGACGACGCTGGGCTGAGCTGTGAAGCTGGAGCTCAGTGAAGCTGCC 120
 QY 121 TGCAGAGGTTATGGCTACACTTTCACCGCTACTGAGTGCATGGGTAAAGAGGCT 180
 Db 121 TGCAGAGGTTATGGCTACACTTTCACCGCTACTGAGTGCATGGGTAAAGAGGCT 180
 QY 181 GGACAGAGCTTGTAGTGTGAGAGATGATTCCTTGAGATTAATTAATTAATTAAT 240

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Db 181 GGAGAGGCGCTGAGTGGATGGAAGATTGATCTCCGATGAGTAAGTCACTACAT 240..
QY 241 CAATAATTCAGAGGAGCCACATGTCAGTACATTTCTCCAGACAGCCTACATG 300
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Db 241 CAGAGTTCAAGAGGACAGGCGCAGCTAGCTATGACAAATCTCCAGACAGCCTACATC 300
QY 301 CAGCTCAGACAGCCTGACATCTGAGAGCTCTCGGCTACTATTGTGCAAGAGGGGTTAC 360
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Db 301 CAACTCAGACAGCCTGACATCTGAGAGCTCTCGGCTACTATTGTGCAAGAGGGGTTAC 360
QY 361 GAGGATGAGGAGCTATGCTATGACTACTGGGGTCAAGCAGCCTCAGTACCTCTCTCA 420
|||
Db 361 CTCG---GGTCTTGTGCTATGAGTACTGAGGCTCAAGCAGCCTCAGTACCTCTCTCA 417
|||
RESULT 11
AF045499 420 bp mRNA ROD 28-FEB-1998
LOCUS Mus musculus 5E3 monoclonal antibody heavy chain variable region,
DEFINITION (IGH) mRNA, partial cds.
ACCESSION AF045499
NID g2906081
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 420)
O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
TITLE Anti-DNA antibodies of normal mice immunized with poly(DC) are
structurally similar to natural autoantibodies
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 420)
O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-1998) Biochemistry, Tufts University School of
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
FEATURES
source 1..420
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/cell_line="spleen cell hybridoma"
/chromosome="12"
/clone="5E3"
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/db_xref="PID:g2906082"
/translation="MGRSCIMFLAATATVHVSQVLOQPGAEIVKPGASVKISCKAS
GYFTSTWMMVAKRPGRLGEMIGRIDPNSGGTKYKRFKSKATLTIVDKSSSTAYMOL
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/gene="IGH"
58..351
V_region /gene="IGH"
352..375
D_segment /gene="IGH"
376..>420
J_segment /gene="IGH"
BASE COUNT 97 a 104 c 121 g 98 t
ORIGIN
Query Match 76.0%; Score 319.2; DB 13; Length 420;
Best Local Similarity 85.0%; Pred. No. 3e-90;
Matches 357; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 ATGGAGTGAAGCTGATCATCTCTTGTGATCAACAGCTACAGTGTCCACTCCAG 60

|||||
Db 1 ATGGAGTGAAGCTGATCATCTCTTGTGATCAACAGCTACAGTGTCCACTCCAG 60
QY 61 GTCCAGTGCAGAGCCTGGGGCTGAGCTGTGAAGCTGGGACTTGAAGTACCTGTC 120
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Db 61 GTCCAGTGCAGAGCCTGGGGCTGAGCTGTGAAGCTGGGACTTGAAGTACCTGTC 120
QY 121 TGCAGGGTTATGCTACCTTCACCTTCACCAAGTACTGATGACACTGGTGAAGAGGCT 180
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Db 121 TGCAGGGTTATGCTACCTTCACCTTCACCAAGTACTGATGACACTGGTGAAGAGGCT 180
QY 181 GGACAGGCTTGTAGTGGATGCGAGAGATTGATCTTCTGAGAGTAATTAATACTACAT 240
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Db 181 GGACAGGCTTGTAGTGGATGCGAGAGATTGATCTTCTGAGAGTAATTAATACTACAT 240
QY 241 CAATAATTCAGAGGAGCCACATGTCAGTACATTTCTCCAGACAGCCTACATG 300
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Db 241 CAGAGTTCAAGAGGAGCCACATGTCAGTACATTTCTCCAGACAGCCTACATG 300
QY 301 CAGCTCAGACAGCCTGACATCTGAGAGCTCTCGGCTACTATTGTGCAAGAGGGGTTAC 360
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Db 301 CAGCTCAGACAGCCTGACATCTGAGAGCTCTCGGCTACTATTGTGCAAGAGGGGTTAC 360
QY 361 GAGGATGAGGAGCTATGCTATGACTACTGGGGTCAAGCAGCCTCAGTACCTCTCTCA 420
|||
Db 361 GATTCAGAGGAGGCGCTGTTGCTTACTGAGGCGCAAGGACTCTGTCACATGTCTCTCA 420
|||
RESULT 12
MUSIGHYXA 1069 bp DNA ROD 29-SEP-1993
LOCUS Mouse (hybridoma 3A112) Immunoglobulin heavy chain variable region.
DEFINITION I09566
ACCESSION g196111
NID
KEYWORDS heavy chain; immunoglobulin; rearranged variable region; variable
region.
SOURCE Mus musculus (strain C57BL/6J, sub-species domesticus) DNA.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 1069)
Rothenfluh,H.S., Taylor,L., Bothwell,A.L., Both,G.W. and
Steele,E.J.
TITLE Somatic hypermutation in 5' flanking regions of heavy chain
JOURNAL antibody variable regions
MEDLINE Eur. J. Immunol. 23 (9), 2152-2159 (1993)
93380482
FEATURES
source 1..1069
/organism="Mus musculus"
/db_xref="taxon:10090"
promoter 461..468
TATA_signal 491..494
mRNA 520..1069
BASE COUNT 272 a 236 c 242 g 313 t 6 others
ORIGIN
Query Match 75.5%; Score 317.2; DB 13; Length 1069;
Best Local Similarity 86.5%; Pred. No. 1.5e-89;
Matches 346; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 21 CTTCTTCTGATCAACAGCTACAAATGTCCATCCAGGTCCAACTGACGAGCCTGG 80
|||
Db 670 CATCACTTTCCTTCTCTCCACAGGTGTCCATCCAGGTCCAACTGACGAGCCTGG 729
QY 81 GAGTACCTTGTGAAGCCTGGGACTCAGTGAAGCTCTCCGCAAGGGTATAGCTACAC 140
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Db 730 GAGTACCTTGTGAAGCCTGGGACTCAGTGAAGCTCTCCGCAAGGGTATAGCTACAC 140
QY 141 CTTACACAGCTACTGATGAGCTGGGTGAAGCAGAGGCTTGAGACAGGCTTGAAGTAT 200
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Db 790 CTCACAGCTACTGTGATGACACGTGGGTGAGAGAGCCCTGGCCAGGCTTGAAGTATG 849
 Qy 201 CGAGAGATGATGATCTTCTGAGAGTAATACATCAATCAAAATTCAGAGGCAAGC 260
 Db 850 TGAAGAGTATGATCTTCTGAGAGTATGATCTTCAATCAATCAAAATTCAGAGGCAAGC 909
 Qy 261 CACATGAGTATGATCAATTTCTCCAGACAGCTTACATGACGTCTACAGAGCTTACATC 320
 Db 910 CACACTGAGTATGACAAACCTCCAGACAGCTTACATGACGTCTACAGAGCTTACATC 969
 Qy 321 TGAGAGCTCTGCGCTCTACTATTTGCAAGAGGGGTACAGAGGATGGATATGATCAT 380
 Db 970 TGAGAGCTCTGCGCTCTACTATTTGCAAGAGGGGTATGCTTCTTACTGCTAT 1029
 Qy 381 TGACTACTGGGTGAGGCAAGGCAAGCTTACAGAGCTTCTCTCA 420
 Db 1030 GGACTACTGGGTGAGGCAAGGCAAGCTTCTCTCA 1069

RESULT 13
 A27941 501 bp DNA PAT 27-JUN-1995
 LOCUS A27941 Coding region for humanised antibody.
 DEFINITION A27941
 ACCESSION A27941
 NID 91248529
 KEYWORDS unidentified.
 SOURCE unidentified
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 501)
 AUTHORS HUMANIZED AND CHIMERIC MONOCLONAL ANTIBODIES
 JOURNAL Patent: WO 9215683-A 31 17-SEP-1992;
 FEATURES Location/Qualifiers
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 /db_xref="taxon:32644"
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 /organism="artificial sequence"
 /db_xref="taxon:29278"
 31..>501
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 /product="humanized antibody"
 /db_xref="PID:e185459"
 /db_xref="PID:g1248530"
 /translation="MGMSYIILFLVATATDVHSQLQPGAEIVKPGASYKLSCKRAS
 GYPTSHMHVVKRAGGLEWIEGFNSNRTYVNEPKSKATLTVDKSSSTAYMQL
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BASE COUNT 127 a 146 c 124 g 104 t
 ORIGIN

Query Match 74.9% Score 314.4; DB 6; Length 501;
 Best Local Similarity 84.3% Pred. No. 1e-88; Mismatches 66; Indels 0; Gaps 0;
 Matches 354; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 1 ATGGGATGAGCTGTATCATCTCTTCTGTATCAACAGCTTACATGCTCCATCCAG 60
 Db 31 ATGGGATGAGCTGTATCATCTCTTCTGTATCAACAGCTTACATGCTCCATCCAG 90
 Qy 61 GTCCAGCTGACAGACCTGGGGCTGAGCTTGTGAAGCCTGGGACTTCACTGAAGCTGTCC 120
 Db 91 GTCCAGCTGACAGACCTGGGGCTGAGCTTGTGAAGCCTGGGACTTCACTGAAGCTGTCC 150
 Qy 121 TGCAAGGCTTATGCTTACACCTTCCAGACGTCTGATGACATGGGTGAAGAGAGGCT 180
 Db 151 TGCAAGGCTTATGCTTACACCTTCCAGACGTCTGATGACATGGGTGAAGAGAGGCT 210
 Qy 181 GGACAGGCTTGTAGTGTGAGAGATGATCTTCTGAGAGTAACTACTACAT 240
 Db 211 GGACAGGCTTGTAGTGTGAGAGATGATCTTCTGAGAGTAACTACTACAT 270
 Qy 241 CAAAATTCAGAGGCAAGGCCACATTTGACTGTAGCATTTCTCCAGACAGCTTACATG 300

Db 271 GAGAAATTCAGAGGCAAGGCCACATGCTGTACAAATCTCCACACAGCTTACATG 330
 Qy 301 CAGCTGACAGCTTGTAGTGTGAGAGATGCTTCTTACTATGTTGCAAGAGGGGTAC 360
 Db 331 CACTGACAGCTTGTAGTGTGAGAGATGCTTCTTACTATGTTGCAAGAGGGGTAC 390
 Qy 361 GAGGATGAGCTTGTAGTGTGAGAGATGCTTCTTACTATGTTGCAAGAGGGGTAC 420
 Db 391 GATTAAGAGGAGGCTTGTAGTGTGAGAGATGCTTCTTACTATGTTGCAAGAGGGGTAC 450

RESULT 14
 126277 501 bp DNA PAT 30-SEP-1996
 LOCUS 126277 Sequence 23 from patent US 5558864.
 DEFINITION 126277
 ACCESSION 126277
 NID 9106147
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 501)
 AUTHORS Bendig, M.M., Kettleborough, C.A. and Saldanha, J.
 JOURNAL Humanized and chimeric anti-epidermal growth factor receptor
 FEATURES Location/Qualifiers
 source 1..501
 /organism="unknown"
 BASE COUNT 127 a 146 c 124 g 104 t
 ORIGIN

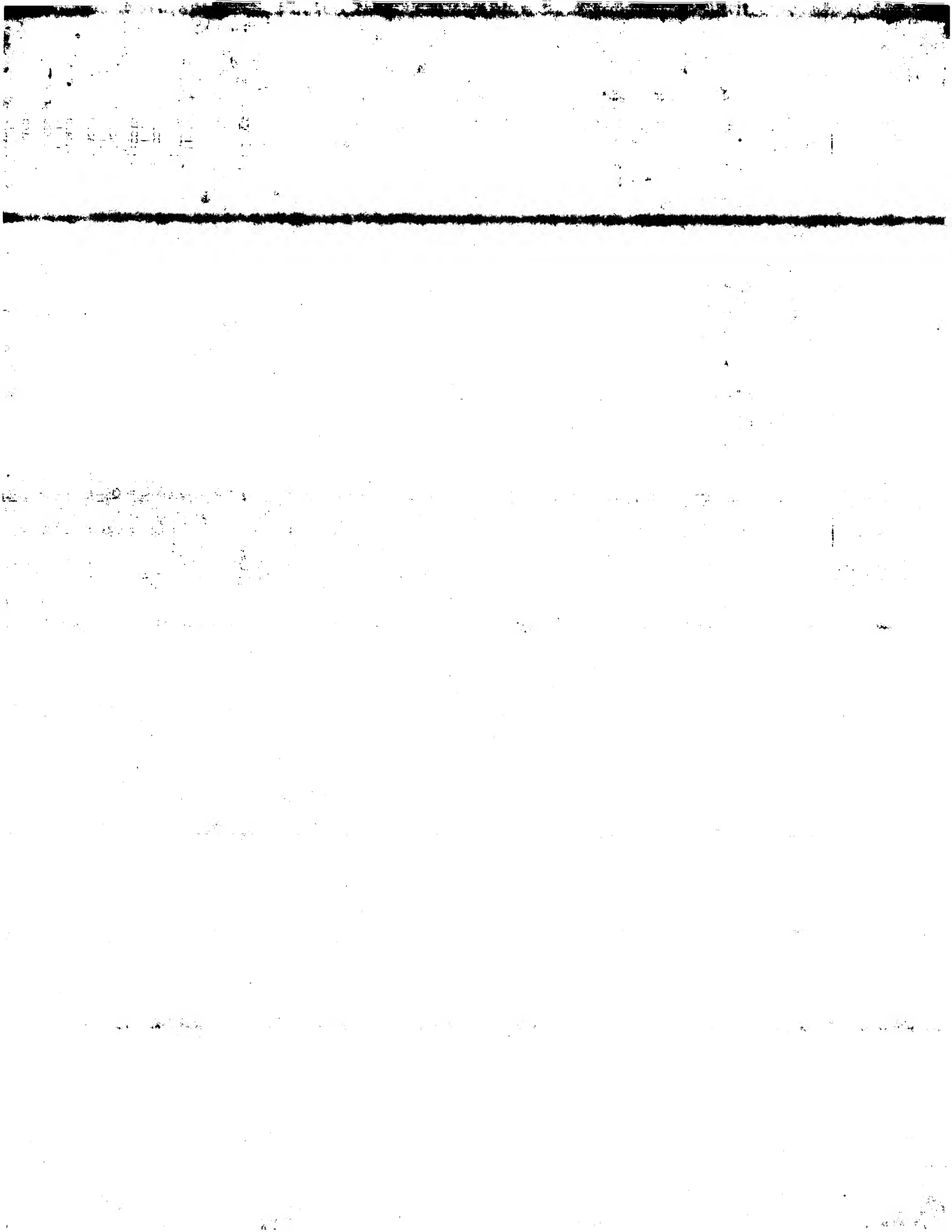
Query Match 74.9% Score 314.4; DB 6; Length 501;
 Best Local Similarity 84.3% Pred. No. 1e-88; Mismatches 66; Indels 0; Gaps 0;
 Matches 354; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 1 ATGGGATGAGCTGTATCATCTCTTCTGTATCAACAGCTTACATGCTCCATCCAG 60
 Db 31 ATGGGATGAGCTGTATCATCTCTTCTGTATCAACAGCTTACATGCTCCATCCAG 90
 Qy 61 GTCCAGCTGACAGACCTGGGGCTGAGCTTGTGAAGCCTGGGACTTCACTGAAGCTGTCC 120
 Db 91 GTCCAGCTGACAGACCTGGGGCTGAGCTTGTGAAGCCTGGGACTTCACTGAAGCTGTCC 150
 Qy 121 TGCAAGGCTTATGCTTACACCTTCCAGACGTCTGATGACATGGGTGAAGAGAGGCT 180
 Db 151 TGCAAGGCTTATGCTTACACCTTCCAGACGTCTGATGACATGGGTGAAGAGAGGCT 210
 Qy 181 GGACAGGCTTGTAGTGTGAGAGATGATCTTCTGAGAGTAACTACTACAT 240
 Db 211 GGACAGGCTTGTAGTGTGAGAGATGATCTTCTGAGAGTAACTACTACAT 270
 Qy 241 CAAAATTCAGAGGCAAGGCCACATTTGACTGTAGCATTTCTCCAGACAGCTTACATG 300
 Db 271 GAGAAATTCAGAGGCAAGGCCACATTTGACTGTAGCATTTCTCCAGACAGCTTACATG 330
 Qy 301 CAGCTGACAGCTTGTAGTGTGAGAGATGCTTCTTACTATGTTGCAAGAGGGGTAC 360
 Db 331 CACTGACAGCTTGTAGTGTGAGAGATGCTTCTTACTATGTTGCAAGAGGGGTAC 390
 Qy 361 GAGGATGAGCTTGTAGTGTGAGAGATGCTTCTTACTATGTTGCAAGAGGGGTAC 420
 Db 391 GATTAAGAGGAGGCTTGTAGTGTGAGAGATGCTTCTTACTATGTTGCAAGAGGGGTAC 450

RESULT 15
 MDSIGHG 471 bp mRNA ROD 15-MAR-1990
 LOCUS MDSIGHG Mouse Ig active mu-chain mRNA V-D-J2-C region, clone 18c10.
 DEFINITION M27788
 ACCESSION M27788
 NID 9195851

KEYWORDS C-region; D-region; J-region; V-region; immunoglobulin heavy chain;
SOURCE Immunoglobulin mu-chain; processed gene.
ORGANISM Mouse spleen, cDNA to mRNA, clone 18C10.
Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 471)
AUTHORS Kaartinen, M., Rocca-Serra, J. and Maekela, O.
TITLE Combinatorial association of V genes: One V-H gene codes for three
non-cross-reactive monoclonal antibodies each specific for a
different antigen (phoxazolone, NP or GAT)
JOURNAL Mol. Immunol. 25, 859-865 (1988)
MEDLINE 89096973
FEATURES
source location/Qualifiers
1..471
/organism="Mus musculus"
/db_xref="taxon:10090"
sig_peptide 49..105
/note="Ig mu-chain signal peptide"
CDS 49..>471
/note="Ig mu-chain V-D-J2-C region precursor"
/codon_start=1
/db_xref="PID:g195852"
/translation="MGWSCIMFLAATATGVSQVQLQPGAEIVKRGASVKLSCKAS
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mat_peptide 106..>471
/note="Ig mu-chain"
BASE COUNT 113 a 126 c 127 g 101 t 4 others
ORIGIN
Query Match 74.5% Score 312.8; DB 13; Length 471;
Best Local Similarity 86.4%; Pred. NO. 3.2e-88;
Matches 363; Conservative 0; Mismatches 42; Indels 15; Gaps 1;
QY 1 ATGGGATGAGCTGTATCATCTCTTCTTGGTATCAACAGCTACAGTGTCCACTCCAG 60
DB 49 ATGGGATGAGCTGTATCATCTCTTCTTGGTATCAACAGCTACAGTGTCCACTCCAG 108
QY 61 GTCCAATGCAAGCAAGCTGGGGCTGAGCTTGTGAAGCTGGGACTTCAGTGAAGCTGTC 120
DB 109 GTCCAATGCAAGCAAGCTGGGGCTGAGCTTGTGAAGCTGGGCTTCAGTGAAGCTGTC 168
QY 121 TGCAGGGTTATGCTACACCTTACACAGCTAGTGAAGTGCATGGGTGAAGCAGAGGCT 180
DB 169 TGCAGGGTTATGCTACACCTTACACAGCTAGTGAAGTGCATGGGTGAAGCAGAGGCT 228
QY 181 GGACAAGGCTTTGAGTGGATGAGAGATGATGATCTTCTGAGAGTAACTAATCTACTACAT 240
DB 229 GGACGAGGCTTTGAGTGGATGAGAGATGATGATCTTCTGAGAGTAACTAATCTACTACAT 288
QY 241 CAAAATTCAGAGGCAAGCAATGACCTAGCTAATCTTCTCCAGCAGCAGCTACATG 300
DB 289 GAGAAAGTCAAGCAAGCAGCAGCTAGCTAATCTTCTCCAGCAGCAGCTACATG 348
QY 301 CAGCTCAGAGGCTGACATCTGAGAGAGCTGCTGCTACTATTGTCAGAGAGGGGTTAC 360
DB 349 CAGCTCAGAGGCTGACATCTGAGAGAGCTGCTGCTACTATTGTCAGAGAGGGGTTAC 408
QY 361 GACGATGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 409 GCCGG-----GGACTACTGGGGCCAGGACACACTCTCAGTCTCTCTCA 453

Search completed: May 11, 1999, 12:00:29
Job time: 1476 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 11:44:10 ; Search time 479.58 Seconds

(Without alignments)
1335.915 Million cell updates/sec

Title: US-08-700-737-14

Perfect score: 420
Sequence: 1 ATGGGATGAGCTGTATCAT.....CTCAGTCACCGTCTCTCA 420

Scoring table: IDENTITY_NUC

Searched: 2002476 segs, 762712212 residues

Database: EST:*

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2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
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8: em_est8:*
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39: em_est17:*
40: em_est18:*
41: em_est19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	238.2	56.7	310	30	A1180569	uc70f09.r
2	215.6	51.3	294	28	A1007196	A1007196 ua73g04.r

3	196.4	46.8	387	22	AA569186	nm30d10.s	
C	4	183.6	43.7	461	31	A1201426	AI201426 gs73c06.x
5	147.8	35.2	279	19	AA300571	AA300571 EST13661	
6	140.4	33.4	431	25	AA710970	AA710970 vt93h09.r	
7	136.8	32.6	287	11	T27609	T27609 EST101034.H	
8	136	32.4	336	29	AA987559	AA987559 or83g01.s	
9	135.2	32.2	291	18	AA377074	AA377074 EST89603	
10	134	31.9	379	21	AA291381	AA291381 zt44g02.r	
11	132.2	31.5	823	16	AA170256	AA170256 ms87g10.r	
12	127.8	30.4	238	11	T29670	T29670 EST89669.Ho	
13	125.8	30.0	265	18	AA377128	AA377128 EST89660	
14	116	27.6	432	31	A1268604	A1268604 q047a10.x	
15	113.6	27.0	372	25	AA581192	AA581192 nd38b11.r	
C	16	104.4	24.9	209	11	T28938	T28938 EST61186.Ho
17	102.4	24.4	198	19	AA383972	AA383972 EST97425	
C	18	97.8	23.3	378	26	AA740786	AA740786 cb32e11.s
19	97.4	23.2	385	11	R86288	R86288 yp12e09.r1	
20	95.2	22.7	630	27	AA895088	AA895088 vy32h01.r	
21	94.2	22.4	330	14	SSCID10	F14516 S.scrofa mr	
22	91.8	21.9	238	21	AA505044	AA505044 aa63g01.r	
23	89.2	21.2	116	30	A1116236	A1116236 ucl8e08.r	
24	89	21.2	419	12	H73816	H73816 vs11b01.r1	
C	25	87.4	20.8	474	31	A1147237	A1147237 qb36f02.x
26	83.4	19.9	432	21	AA544384	AA544384 vk33f04.r	
C	27	80.4	19.1	488	29	AA948436	AA948436 on67a01.s
28	80	19.0	304	17	AA300945	AA300945 EST13823	
29	79.2	18.9	364	16	AA098196	AA098196 mn86h06.r	
30	78	18.6	430	11	R72787	R72787 yj91h09.r1	
31	75.2	17.9	403	26	AA715258	AA715258 nv35a08.r	
32	74.8	17.8	299	11	T27727	T27727 EST13874.Ho	
33	73.4	17.5	597	20	AA472093	AA472093 vhl0a05.r	
34	72.6	17.3	415	22	AA575218	AA575218 vhl0a01.r	
35	72.2	17.2	297	11	T27868	T27868 EST18962.Ho	
36	71.8	17.1	266	24	AA402547	AA402547 zu47h07.r	
C	37	71	16.9	247	27	AA897116	AA897116 am08b07.s
C	38	70.8	16.9	485	29	AA988730	AA988730 or79h12.s
39	70.4	16.8	303	11	R83139	R83139 yp11g03.r1	
40	66.4	15.8	258	18	AA360195	AA360195 EST69374	
41	65.8	15.7	478	11	H43753	H43753 yp21g01.r1	
42	65.2	15.5	278	19	AA381086	AA381086 EST94138	
43	64.6	15.4	273	17	AA300982	AA300982 EST13889	
44	62	14.8	280	17	AA326955	AA326955 EST30467	
45	61	14.5	426	30	A1124611	A1124611 am59d10.x	

ALIGNMENTS

RESULT 1
LOCUS A1180569
DEFINITION uc70f09.r1 Soares mouse mammary gland NbmMG Mus musculus CDNA clone 1431017 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376 Mouse Immunoglobulin H-chain V-region pseudogene mRNA, complete (MUSE);, mRNA sequence.

ACCESSION A1180569
NID 93731207
KEYWORDS EST

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 310)

AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacey, M., Le, M., Martin, J., Morris, M., Scheinberg, K., Steptoe, M., Tan, F., Underwood, R., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project

RESULT	3
AA569186	
LOCUS	
DEFINITION	aa569186 387 bp mRNA EST 09-SEP-1997
ACCESSION	mm00d10.s1 NCI-CGAP.Lip2 Homo sapiens cDNA clone IMAGE:1061683
NID	similar to g9:L02325 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);
KEYWORDS	mRNA sequence.
SOURCE	AA569186
ORGANISM	g2342240
	EST.
	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
TITLE	Primates; Catarrhini; Hominoide; Homo.
COMMENT	1 (bases 1 to 387)
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
	Tumor Gene Index
	Unpublished (1997)
CONTACT:	Robert Strausberg, Ph.D.
TEL:	(301) 496-1550
EMAIL:	Robert.Strausberg@nih.gov
TISSUE	Procurement: L. Jeffrey Medeiros, M.D., Michael R.
	Emmert-Buck, M.D., Ph.D.
CNA	Library Preparation: David B. Krizman, Ph.D.
CNA	Library Arrayed by: Greg Lennon, Ph.D.
DNA	Sequencing by: Washington University Genome Sequencing Center
clone	distribution: NCI-CGAP clone distribution information can be
found	through the I.M.A.G.E. Consortium/MLND at:
www-bio.liml.gov/db/rp/image/Image.html	
Insert Length:	1722 Std Error: 0.00
Seq primer:	-40m13 fwd. Err from Amersham
High quality	sequence stop: 284.
FEATURES	
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/organism=	"Homo sapiens"
/note=	"Vector: pAMP10; mRNA made from liposarcoma, CDNA
made by	oligo-dt priming. Non-directionally cloned.
size-selected	on agarose gel, average insert size 600 bp.
Reference:	Krizman et al. (1996) Cancer Research
56:3380-5383."	
/db_xref=	"taxon:9606"
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ORIGIN	

	Query Match	46.8%	Score 196.4	DB 52	Length 387
	Best Local Similarity	72.6%	Pred. No. 5.7e-52		
	Matches 254	Conservative 0	Mismatches 96	Indels 0	Gaps 0
OY	1 ATGGATGAGAGCTGTATCATCTCTTCTTGTATCAACAGCTACAGAGTGTCCACTCCAG	60			
Db	38 ATGGACTGGACCTGGAGGGCTTCTTGCTTGTCTGGCTGTAGCTCCAGAGTCTCATCCAG	97			
OY	61 GTCCACATGACACGACCTGGGGCTGGAGCTGTGAAGCCGAGGACCTCACTGAAGCTGCC	120			
Db	98 GTCCACATGTGTCACTCTGGGGCTGTGAAGCAAGCTCGGGGCTCACTGAAGCTTTC	157			
OY	121 TCCAAAGGTTATGCTACACCTTCACACGCTACTGGATGCTACTGGGTGAAGCAGGCCCT	180			
Db	158 TGTAAAGCATCTGGGATTCACCTCCACCAACTCCCATATGACTGGGTGGCAAGGCCCT	217			
OY	181 GGACAGAGGCTTGAGAGTGATGGAGAGATGTTATTCCTTCGAGAGTAATCTAATCAAT	240			
Db	218 GGGCAAGGCTTGAGATGGGTGGGAATGATCAATTTCTAGTAGTGTATATTAAGTAAGCA	277			
OY	241 CAAAAATTCAGGGCAGAGCCACATTGACTGTAGACATTTCTCCAGCAGACCTTCATG	300			

DB	278	CAGAGTTCGAGGGGAGAGTCAACATGACACAGGACAGCTCCACAGACAGACTCTATATG	337
QY	301	CAGCTCAGCAGCCTGACATCTGAGGAGCTCTGCGGTCTACTATTGTGCA	350
Db	338	GAGCTTACAGAGCTGAGATCTGAGAGACAGGCGCTCTATTACTGTGCG	387
RESULT	4		
LOCUS	AI201426/c		
DEFINITION	AI201426 461 bp mRNA EST 30-OCT-1998		
ACCESSION	957306.x1 NCI-CGAP_P128 Homo sapiens cDNA clone IMAGE:1943722		
NID	93754032		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
AUTHORS	Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 461)		
COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
FEATURES	Tumor Gene Index		
source	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	unknown library type		
	Insert Length: 608 Std Error: 0.00		
	Seq primer: -40UP from GlbDc.		
	Location/Qualifiers		
	1. 461		
	/organism="Homo sapiens"		
	/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)		
	with a modified polylinker; Plasmid DNA from the		
	normalized library NCI-CGAP_P122 was prepared, and ss		
	circles were made in vitro. Following HAP purification,		
	this DNA was used as tracer in a subtractive hybridization		
	reaction. The driver was PCR-amplified cDNAs from a pool		
	of 5,000 clones made from the same library (clones		
	985608-986759, 1101192-1101959, and 121928-1220615).		
	Subtraction by Bento Soares and M. Fatima Bonaldo."		
	/db_xref="taxon:9606"		
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	/clone_lib="NCI-CGAP_P128"		
	/sex="male"		
	/dev_stage="adult"		
	/lab_host="DH10B"		
BASE COUNT	93 a 132 c 106 g 130 t		
ORIGIN			
Query Match	43.7%; Score 183.6; DB 31; Length 461;		
Best Local Similarity	73.6%; Pred. No. 6.6e-48;		
Matches	234; Conservative 0; Mismatches 84; Indels 0; Gaps 0;		
QY	35	CACACGCTACAGAGTGTCCACTCCACAGTCCACAGCTGACAGACCTGGGGCTGAGCTTGTGA	94
Db	461	CACACGCTACAGAGTGTCCACTCCACAGTCCACAGCTGACAGACCTGGGGCTGAGTGAAGA	402
QY	95	AGCGCGGACCTTCAGTGAAGCTGCTCCAGAGGGTATAGCTACACCTTCACACACTACT	154
Db	401	AGCGCGGCGCTTCAGTGAAGGCTCTCCACAGGCTTCGAGTACATCTTCACCGCTACT	342
QY	155	GGATGACATGGGTGAGAGAGAGCTGACAGAGGCTTGATGGATCGAGAGATTGATC	214
Db	341	ATATGCAATGGGTGAGAGAGGCGCTTGACAGAGACTTGGGTGATGGAGAGATCAACC	282
QY	215	CTTCTGAGAGTATATCTACTACATCAAAAATTCAAGGGCAGAGGCCATTTGACTGTG	274

Db	281	CTAACAGGGGGGCAACAACATATCACAGAAAGTTTTCAGGGCGAGAGTCACCATGACCAAGG	222
QY	275	ACATTTCCCTCCAGCACAAGCCATACATGCAGGTCACAGCCTCGATCATCGAGAGCTTCGCG	334
Dd	221	ACAGCTCCATAGAGCACAAGCCATACAGGAGGTCGAGACCACTCGAGATCTGAGAGCACAGGCCA	162
QY	335	TCCTACTATTCGCAAGG	352
Dd	161	CGATTTACTGTCGAGAG	144

RESULT	5
AA300571	
LOCUS	AA300571 279 bp mRNA
DEFINITION	EST1361 Testis tumor Homo sapiens CDNA 5' end similar to similar to immunoglobulin mu heavy chain, VDJC regions (GB:M18512), mRNA sequence.

ACCESSION	AA300571
NID	g1953132
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

Eukaryotes; eukaryotes; metazoa; chozoata;
vertebrata; mammalia; eutheria; primates; catarrhini; hominidae;
homo.

REFERENCE	AUTHORS
1 (pages 1 to 2/9)	
	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
	Balt, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D.,
	White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Well, C.,
	Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
	Fitzgerald, L.M., Fitzhugh, W.M., Fitchman, J.L., Geopjanen, N.S.,
	Glock, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkley, P.S., Jr.,
	Kelley, M.M., Kelley, J.C., Liu, Y.-I., Marmaros, S.M., Merrick, J.M.,
	Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
	Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, R.,
	Small, K.V., Spitzigs, T.A., Utterback, T.R., Weldman, J.F., Li, Y.,
	Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
	Dinke, D., Feng, D.-F., Fertile, A., Fischer, C., Hastings, G.A.,
	He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
	Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisener, P.S., Olsen, H.,
	Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
	Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
	Fraser, C.M., and Venter, J.C.
TITLE	
JOURNAL	Initial assessment of human gene diversity and expression patterns
MEDLINE	based upon 83 million nucleotides of cDNA sequence
COMMENT	Nature 377 (6547 Suppl), 3-174 (1995)
	Other_Ensts: TH0165571

Contact: Kerilavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel.: 3018699056
Fax: 3018699423
Email: arkerilavet@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hg1/hg1.html>)
Seq primer: M13 Reverse.

FEATURES	location/qualifiers
source	1. .279

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/organism="Homo sapiens"
/organ="testis; Vector: pBluescript SK-; Site_1
ECORI: Site 2. XhoI"

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/clone_lib="Testis"
/sex="male"
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MRNA	63 a	74 c	85 a	56 t	1 others
BASE COUNT	63 a	74 c	85 a	56 t	1 others
dev_stage="adult"	<1	>279			

the Not I and Eco RI sites of the modified pRT73 vector.

Query Match	35.28	Score	147.8	DB	17	Length	279
Best Local Similarity	74.68	Pred	No. 1.2e-36				
Matches	185	Conservative	0	Mismatches	63	Indels	0
						Gaps	0

Qy	1	ATGGGATGAGAGCTGTATCATCTCTTCTTGGTATCAACAGCTACAGTGTCCACTCCAC	60
Db	32	ATGAGCTGGAGCTCGGAGGATCTCTTCTTGGTGGGAGCAGCCACAGAGGCCCTCCAG	91
Qy	61	GTCGAATGTGAGCAGCCTGGGCGTGGAGCTTGGAAGCCTGGGACTTCAGTGAAGCTGCC	122
Db	92	GTCGAGCTGGTGGAGTCTGGGGCTAGAGTGAAGAAGCCTGGGGGCTCAGTAAGGTCTCC	153
Qy	121	TGCAAGGTTATGGCTACACCTTTACACAGCTACTGTGATAGCACTGGGTGAAGCAGAGGCT	182
Db	152	TGCAAGGCTTCTGGATACACCTTACCGGCTACTATATGCACTGGGTCAGCAAGGCCCT	213
Qy	181	GGACAAAGCCTTGAATGGATCGGAGAGATGTGATCTTCTTGAGACTAAATACTACAAAT	242
Db	212	GGACAAAGGCTTNAAGTGGATGGATGGATGCAATCAACCTAAAGTGGTGGCACAACCTATGCA	273
Qy	241	CAAAATTT 248	
Db	272	CAGAGATT 279	

RESULT	6
AA710970	
LOCUS	
DEFINITION	AA710970 431 bp mRNA
	vt33b09.r1 Soares mouse mammary gland NbMG Mus musculus cDNA clone
	118753 5' similar to gb:M1852 IG HEAVY CHAIN PROCURSOR V-I REGION
	(HbMA); gb:x70423 M.musculus mRNA for monoclonal antibody heavy
	chain gamma (MOUSE); mRNA sequence.

ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AA/10970	92720888	EST.	house mouse.	Mus musculus	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 431)	Matra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., . . .		
						Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelings, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and Waterston, R.	The WashU-HWU Mouse EST Project		Unpublished (1996)

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:636601
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 198.

FEATURES

source

/organism='Mus musculus'
/strain='C57BL/6J'

/note='Organ: mammary gland; Vector: pT7 π 3D-Pac
(Pharmacia) w/ta modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
o14go(gt) primer [5],
TGTTACCAATCTGAGTAGCGAGCCGCCGAATGTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested w/Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.

Saudek, D.M., Shirley, R., Smail, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A.,

JOURNAL COMMENT

1111b National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Db 255 CAGAACTTCGGGGAGAGATCACCCTGACCGAGCA 291

RESULT 10
AA291381
LOCUS
DEFINITION
AA291381 379 bp mRNA EST 08-AUG-1997
2744902.r1 Soares ovary tumor NBH07 Homo sapiens cDNA clone 725234
5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION
(HUMAN); mRNA sequence.

ACCESSION
AA291381
NID
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;

REFERENCE
AUTHORS
1 (bases 1 to 379)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
Washu-Merck EST project
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1576 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 361.
Location/Qualifiers
1. 379
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT7/3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone_id="725234"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/dev_stage="4 weeks"

BASE COUNT 85 a 82 c 121 g 91 t

ORIGIN
mRNA
BASE COUNT 85 a 82 c 121 g 91 t

Query Match 31.9%; Score 134; DB 21; Length 379;
Best Local Similarity 66.1%; Pred. No. 2.9e-32;
Matches 209; Conservative 0; Mismatches 105; Indels 2; Gaps 1;

Db 37 ACACCTACAGTGTCCACTCCAGTCACTGACAGCCTGGGCGTGAAG 96
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
13 ACACCTACAGTGTCCACTCCAGTCACTGACAGCCTGGGCGTGAAG 72
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
97 CCTGGAGCTTCACTGAGAGCTGTCTCGAAGGGTATGAGCTACACCTACTGG 156
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 73 CTGGGGCC--CAGTGAAGGCTCTCTGTAAGACCTGTGTTACACTTTGGCACTTTTGGT 130
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
97 ATGCACTGGGTGAAGCAGAGCCCTGGAGACAGGCTTGTGATCGAGAGATTGATCTT 216
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 131 ATCACTGGGTGGCGGAGGCCCTTGACCAAGGCTTGATGATGGAGATCAGCGTT 190

RESULT 11
AA170256
LOCUS
DEFINITION
AA170256 823 bp mRNA EST 16-FEB-1997
ms87910.r1 Soares mouse 3NBMS Mus musculus cDNA clone 618594 5'
similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION (HUMAN);
gb:V00821 Mouse mRNA fragment for immunoglobulin mu encoding the
C-terminus (MOUSE); mRNA sequence.

ACCESSION
AA170256
NID
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE
AUTHORS
1 (bases 1 to 823)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacey, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Thelning, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The Washu-HMI Mouse EST Project
Unpublished (1996)

TITLE
JOURNAL
COMMENT
Contact: Marra M/Mouse EST Project
Washu-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:379418
Putative full length read
vector to vector length is 867
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 492.
Location/Qualifiers
1. 823
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT7/3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:10090"
/clone_id="618594"
/clone_id="618594"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"

FEATURES
source

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 12:03:26 ; Search time 88.51 Seconds

(without alignments)
892.725 Million cell updates/sec

Title: US-08-700-737-14

Perfect score: 420
Sequence: 1 ATGGGATGAGCTGTATCAT.....CCTCACTACCGCTCTCTCA 420

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database: N_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	420	100.0	420	1	V20078	DNA encoding murin
2	416.4	99.1	494	1	V20085	Consensus DNA sequ
3	406.2	96.7	428	1	V20089	DNA sequence of mu
4	359.2	85.5	540	1	V20076	DNA encoding the h
5	335.8	80.0	1582	1	O94037	Mab 55.1 heavy cha
6	330.4	78.7	458	1	Q15164	VH186 region of an
7	327.2	77.9	429	1	T05312	MAB SCH94.03 heavy
8	314.4	74.9	501	1	Q28739	CDNA of VH425 anti
9	308.4	73.4	499	1	T38509	Heavy chain coding
10	298	71.0	420	1	T36303	Anti-hepatitis B h
11	298	71.0	420	1	T36304	Anti-hepatitis B h
12	298	71.0	420	1	V18553	Human anti-hepatit
13	298	71.0	433	1	V18554	Human anti-hepatit
14	298	71.0	433	1	V03866	Human anti-hepatit
15	298	71.0	420	1	V03836	Human anti-hepatit
16	298	71.0	420	1	V18589	Human anti-hepatit
17	298	71.0	433	1	V18590	Human anti-hepatit
18	296.4	70.6	420	1	N70967	Sequence of the an
19	296.4	70.6	420	1	N70968	Sequence of the an
20	296.4	70.6	420	1	T51039	Chimeric anti-hepa
21	296.4	70.6	433	1	T70857	Mouse-human chimae
22	296.4	70.6	420	1	T70858	Mouse-human chimae
23	294.4	70.1	3058	1	T77137	Single chain anti
24	293.6	69.9	357	1	T04016	Anti-EGFR antibody
25	293	69.8	357	1	T43805	Anti-DNA antibody
26	292	69.5	477	1	O12057	Sequence encoding
27	292	69.5	477	1	O12013	Sequence encoding
28	290.8	68.5	1284	1	T77139	Single chain anti
29	287.6	68.5	440	1	V22074	DNA encoding the h
30	287.2	68.4	471	1	T43438	Mab Co-1 heavy cha
31	283	67.4	416	1	T85854	Anti-HMG MAB CTMO
32	282.4	67.2	471	1	O08607	Co-1 Heavy Chain V
33	282.4	67.2	357	1	T58252	Lead binding Mab 8
34	281.8	67.1	357	1	T04014	Anti-EGFR antibody
35	281.4	67.0	416	1	O38877	CTMO1 VH cDNA. Ant
36	280.6	66.8	1553	1	O79930	Anti-tobacco mosai
37	280.2	66.7	858	1	O64817	PRAS11 between H1
38	280.2	66.7	858	1	O70658	SCFV PRAS107 and p
39	280.2	66.7	1356	1	O70659	SCFV PRAS108 and p
40	280.2	66.7	1257	1	O70661	SCFV PRAS110 and p
41	280.2	66.7	1259	1	O70662	SCFV-BSRase fusio
42	280.2	66.7	1648	1	O70665	SCFV-DNaseI fusion
43	279.2	66.5	411	1	V12263	Monoclonal antibod

ALIGNMENTS

RESULT	1	
V20078		
ID	V20078	standard; DNA; 420 BP.
AC	V20078:	
DT	14-JUL-1998	(first entry)
DE	DNA encoding murine Act-1 heavy chain variable region.	
Mouse:	Act-1 antibody; human alpha4-beta7 integrin;	
KW	Muscosal adressin cell adhesion molecule-1; MadCAM-1;	
KW	humanised antibody; murine antigen binding region; inhibition;	
KW	leukocyte infiltration of tissue; treatment; inflammatory disease;	
KW	inflammatory bowel disease; ss.	
OS	Mus sp.	
FH	Key	Location/Qualifiers
FT	CDS	1..420
FT		/*tag= a
FT	sig_peptide	1..57
FT		/*tag= b
FT	mat_peptide	58..420
FT		/*tag= c
PN	MO9806248-AZ.	
PD	19-FEB-1998	
PF	06-AUG-1997; U13884.	
PR	15-AUG-1996; US-700737.	
PA	(LEUK-) LEUKOSITE INC.	
PI	Bending M, Jones ST, Newman W, Ponath PD, Ringler DJ,	
PI	Saldanha J	
DR	WPI: 98-159172/14.	
P-PSDB:	W53815.	
DR	Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -	
PT	used for treating inflammatory disease, pancreatitis, diabetes,	
PT	asthma, graft versus host disease and sarcoidosis	
PS	Claim 30; Fig 9; 145pp: English.	
CC	The present sequence encodes the heavy chain variable region of	
CC	murine antibody Act-1. Act-1 is active against human alpha4-beta7	
CC	integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a	
CC	ligand of this particular integrin. The Act-1 antibody interferes with	
CC	alpha4-beta7 integrin binding to MadCAM-1, which is present of high	
CC	endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used	
CC	to inhibit the interaction of cells bearing alpha4-beta7 with cells	
CC	bearing a ligand for alpha4-beta7. It can be used for inhibiting	
CC	leukocyte infiltration of tissues, e.g. for treating inflammatory	
CC	diseases such as inflammatory bowel disease. The immunoglobulin can	
CC	also be used for detection, isolation and diagnosis.	
SQ	Sequence	420 BP; 104 A; 106 C; 112 G; 98 T;
Query Match	100.0%;	Score 420; DB 1; Length 420;
Best Local Similarity	100.0%;	Pred. No. 4.9e-109;
Matches	420; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	ATGGGATGAGCTGTATATCTCTCTTCTGGATATCAACAGCTACAGTCTCCACTCCGAG 60
DB	1	ATGGGATGAGCTGTATATCTCTCTTCTGGATATCAACAGCTACAGTCTCCACTCCGAG 60
QY	61	GTCACACTGCACACACCTGGGGCTGAGCTTGGAAGCCCGGAGCTTCAGTGAAGCTGTCC 120
DB	61	GTCACACTGCACACACCTGGGGCTGAGCTTGGAAGCCCGGAGCTTCAGTGAAGCTGTCC 120
QY	121	TGCAGGGTTATGCTACACCTTCACACAGCTACTGGATCAGTGGGTGAAGCAGAGGCTT 180
DB	121	TGCAGGGTTATGCTACACCTTCACACAGCTACTGGATCAGTGGGTGAAGCAGAGGCTT 180
QY	181	GGACAAAGGCTTGAATGGATGGAGAGATATCTCTTCGAGAGTAATCTAACTAACAAT 240
DB	181	GGACAAAGGCTTGAATGGATGGAGAGATATCTCTTCGAGAGTAATCTAACTAACAAT 240

Qy	241	CAAAATTCAGGGGAAAGGCCACATTGACTCTAAGACATTTCTCTACACACAGCCTAATG	300
Db	241	CAAAATTCAGGGGAAAGGCCACATTGACTCTAAGACATTTCTCTACACACAGCCTAATG	300
Qy	301	CAGCTCAGCAGCCTGCATCTGAGGACCTCTGGGCTCTATTGTGCAAGAGGGGGTTAC	360
Db	301	CAGCTCAGCAGCCTGCATCTGAGGACCTCTGGGCTCTATTGTGCAAGAGGGGGTTAC	360
Qy	361	GACGATGGGACTATGCTATTGACTACTGCGGGTCAAGGACACTCAGTCACCGTCTCTCA	420
Db	361	GACGATGGGACTATGCTATTGACTACTGCGGGTCAAGGACACTCAGTCACCGTCTCTCA	420

RESULT 2

ID	V20085; standard; DNA; 494 bp.
AC	V20085;
DT	14-Jul-1998 (first entry)
DE	Consensus DNA sequence of the murine variable heavy chain region.
KW	Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW	Muscle; adhesion molecule-1; MadCAM-1;
KW	humanised antibody; murine antigen binding region; inhibition;
KW	leukocyte infiltration of tissue; treatment; inflammatory disease
KW	inflammatory bowel disease; ss.
OS	Mus sp.

	Location/Qualifiers
FH	Key
FT	CDS
	13. .445

FT	/*tag-	codon	given"
FT	/note-	"no stop	
FT	/trans-	except-	(pos: 16. 18. aa: Xaa
FT	/trans-	except-	(pos: 19. 21. aa: Xaa
FT	/trans-	except-	(pos: 22. 24. aa: Xaa
FT	/trans-	except-	(pos: 25. 27. aa: Xaa
FT	/trans-	except-	(pos: 28. 30. aa: Xaa
FT	/trans-	except-	(pos: 31. 33. aa: Ile
FT	/trans-	except-	(pos: 34. 36. aa: Xaa

FT	sig_peptide
FT	
FT	mat_peptide

ET WO9806248-A2
PN

PD 19-FEB-1998.
PF 06-AUG-1997; 013884.

PR 15-AUG-1996; US-7007
PA (LEUK-) LEUKOSITE IN

PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
PI Saldanha J;

DR WPI; 98-159172/14.
DR P-PSDB; W53816.

PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes

PT asthma, graft versus host disease and sarcoidosis
Example 1: Ftd 1: 145p: English.
PS

The present sequence represents the

several independent mouse heavy chain variable region clones. Act-1 is active against human alpha4-beta2 integrin. Muscros) adrenocta cell

adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin

line act-1 antibody interferes with alpha₂-beta₁ integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal

CC lymph nodes: variable regions were amplified from DNA encoding Act-1.
CC using degenerate PCR primers V20079-02. The degeneracy of the PCR primers

cc produced several different sequences, of which the present sequence is a
cc consensus sequence. The present sequence was used to construct

cc chimeric, humanised Act-1 antibodies, which contain murine antigen binding regions. The humanised immunoglobulin can be used to inhibit

cc the interaction of cells bearing alpha4-beta7 with cells bearing a
cc ligand for alpha4-beta7. It can be used for inhibiting leukocyte

cc infiltration of tissues, e.g. for treating inflammatory diseases such
cc as inflammatory bowel disease. The immunoglobulin can also be used for

CC	detection, isolation and diagnosis.	
5Q	Sequence	113 A; 120 C; 118 G; 104 T;

Query Match	99.18;	Score 416.4;	DB 1;	Length 494;
Best Local Similarity	97.98;	Pred. No. 5.2e-108;		
Matches 411; Conservative	9;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGGGATGGAGCCTTATCATCCCTCTCTTGGTATACAGACCTCAACAGTGCACCTCCAG	60
Db	13	ATGGATATGASACTCKKTKATATTTCTTTGGTATCAACAGCTCAACAGTGCACCTCCAG	72
QY	61	GTCCAACTGCAGCAGCCTGGGGGCTGAGCTTGTGAAGCTGGGACTTCAGTGAAGCTGCC	120
Db	73	GTCCAACTGCAGCAGCCTGGGGGCTGAGCTTGTGAAGCTGGGACTTCAGTGAAGCTGCC	132
QY	121	TGCAAGGTTATGGCTACACCTTCACCAGCTACTGGATGCACCTGGGTGAAGCAGAGGCT	180
Db	133	TGCAAGGTTATGGCTACACCTTCACCAGCTACTGGATGCACCTGGGTGAAGCAGAGGCT	192
QY	181	GGACAAGGCTTGATGGATGCGGAGATTTGATCCCTCAGAGTAATACTACTCAAT	240
Db	193	GGACAAGGCTTGATGGATGCGGAGATTTGATCCCTCAGAGTAATACTACTCAAT	252
QY	241	CAAAATTCAGAGGCGACACATTGACTGTAGACATTTCCTCCAGCAGAGCTCATG	300
Db	253	CAAAATTCAGAGGCGACACATTGACTGTAGACATTTCCTCCAGCAGAGCTCATG	312
QY	301	CAGCTCAGCAGCCTGACATCTGAGGACTCTGGCGTCTACTATTGTGCMAAGGGGGTTAC	360
Db	313	CAGCTCAGCAGCCTGACATCTGAGGACTCTGGCGTCTACTATTGTGCMAAGGGGGTTAC	372
QY	361	GAGCGATGGGACTATGCTATTGACTACTGGGGTCAAGGCAACCTCAGTCAACCGTCTCTCA	420
Db	373	GAGCGATGGGACTATGCTATTGACTACTGGGGTCAAGGCAACCTCAGTCAACCGTCTCTCA	432

RESULT 3

V20089
ID V20089 standard; DNA; 428 BP.

AC	V20089;
DT	14-JUL-1998 (first entry)

DE DNA sequence of murine variable heavy chain region of clone H2B#34.
KM Mouse; Act-1 antibody; human alpha4-beta7 integrin;

KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KW humanised antibody; murine antigen binding region; tr

KW leukocyte infiltration of tissue; treatment; inflammatory disease, inflammatory bowel disease: ss.

OS	Mus sp.	Location/Qual
FH	Key	

FT	18.428
FT	/tag= a
CDS	

	/	no stop codon given
WT	/note=	"no stop codon given"
PN	W098063A8-A2	

PD 19-FEB-1998.
06-AUG-1997: #13894

PR 15-AUG-1996; US-700737.
PR (FEB-) FERTOSTE INC

PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ
 (LEOR-) LEUCOSILE INC.

PI Salanna J;
DR WPI; 98-159172/14

DR	p-PSDB; W53818.
PT	Humanised immunoglobulin reactive with alpha-4-beta-7 integrin

PT used for treating inflammatory disease, pancreatic
asthma, graft versus host disease and sarcoidosis

PS Example 1; Fig 2; 145pp; English.
CC The present sequence represents the nucleotide sequence comprising the

CC variable region of murine Act-1 antibody determined from clone H2B334.
CC Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin

cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody interferes with alpha4-beta7 integrin binding

to Madcam-1, which is present of high endothelial venules in mucosal lymph nodes. The present sequence was used to construct chimeric.

CC The humanised immunoglobulin can be used to inhibit the interaction of

PR 03-JUN-1994; GB-011089.
 PA (ZENE) ZENECA LTD.
 PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
 PI Rose MS, Wright AF;
 DR WPI: 95-215262/28.
 P-PSDB: R76088.
 PT Antigen binding structures containing CDRs recognising the CA55.1
 PT antigen - produced by hybridomas and host cells, for use in the
 PT diagnosis and therapy of cancer
 PS Disclosure: Fig.15; 11pp: English.
 CC Mab 55.1 (ECCACC 93081901) recognises the colorectal tumor-associated
 CC antigen CA55.1. CDNA for the heavy (094037) and light (094036)
 CC chains of 55.1 were isolated, and F(ab)'2, Fab, Fv, scFv or
 CC V-min humanized 55.1 constructs have been expressed in myeloma
 CC cells and E. coli.
 SQ Sequence 1582 BP: 405 A; 466 C; 379 G; 332 T;

Query Match 80.0%; Score 335.8; DB 1; Length 1582;
 Best Local Similarity 87.6%; Pred. No. 2.8e-85;
 Matches 367; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 ATGGATGAGAGCTGTATCACTCTTCTTGTGTATCAACAGCTCAAACTGCTCCAG 60
 DB 54 ATGGATGAGAGCTGTATCACTCTTCTTGTGTATCAACAGCTCAAACTGCTCCAG 113
 QY 61 GTCCAACTGACAGAGCTGGGGCTGAGCTTGTGAAGCTGGAGCTTCAAGCTGTC 120
 DB 114 GTCCAACTGACAGAGCTGGGGCTGAGCTTGTGAAGCTGGAGCTTCAAGCTGTC 173
 QY 121 TGCAGAGCTTATGCTACCTTACACAGCTTGTGATGATGAGCTGGTGAAGAGGCT 180
 DB 174 TGCAGAGCTTATGCTACCTTACACAGCTTGTGATGATGAGCTGGTGAAGAGGCT 233
 QY 181 GGAAGAGCTTATGCTACCTTACACAGCTTGTGATGATGAGCTGGTGAAGAGGCT 240
 DB 234 GGAAGAGCTTATGCTACCTTACACAGCTTGTGATGATGAGCTGGTGAAGAGGCT 293
 QY 241 CAAATATTCAGAGGCAAGGCACTTGTGATGATGAGCTGGTGAAGAGGCT 300
 DB 294 GAGAGAGCTTCAAGAGGCAAGGCACTTGTGATGATGAGCTGGTGAAGAGGCT 353
 QY 301 CAGCTGAGAGCTTCAAGAGGCAAGGCACTTGTGATGATGAGCTGGTGAAGAGGCT 360
 DB 354 CAGCTGAGAGCTTCAAGAGGCAAGGCACTTGTGATGATGAGCTGGTGAAGAGGCT 413
 QY 361 GAGGAGAGGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
 DB 414 TATGATTACGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 472

RESULT 6
 ID Q15164 standard; DNA; 458 BP.
 AC Q15164;
 DT 16-MAR-1992 (first entry)
 DE VH186 region of anti-nitrophenylacetyl heavy chain Ab gene.
 KM mouse; murine; antibody; heavy chain; variable region;
 OS polymerase chain reaction; ss.
 PN Mus musculus.
 PD J03247283-A.
 PF 09-NOV-1991.
 PR 29-DEC-1989; 340628.
 PA (MAYO) MATSUSHITA ELEC IND KK.
 DR WPI: 91-366330/50.
 PT DNA binding to terminal of anti-nitrophenylacetyl antibody gene
 PT - allows specific amplification of variable region in gene by PCR
 PS Disclosure: Page 2; 3pp: Japanese.
 CC This sequence corresponds to the region of the heavy chain variable
 CC region of the murine anti-nitrophenylacetyl IgG antibody which is
 CC amplified by PCR primers HA and HS.
 CC See Q15159-Q15163.

SQ Sequence 458 BP: 112 A; 124 C; 120 G; 102 T;

Query Match 78.7%; Score 330.4; DB 1; Length 458;
 Best Local Similarity 88.3%; Pred. No. 6.4e-84;
 Matches 371; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 1 ATGGATGAGAGCTGTATCACTCTTCTTGTGTATCAACAGCTCAAACTGCTCCAG 60
 DB 1 ATGGATGAGAGCTGTATCACTCTTCTTGTGTATCAACAGCTCAAACTGCTCCAG 60
 QY 61 GTCCAACTGACAGAGCTGGGGCTGAGCTTGTGAAGCTGGAGCTTCAAGCTGTC 120
 DB 61 GTCCAACTGACAGAGCTGGGGCTGAGCTTGTGAAGCTGGAGCTTCAAGCTGTC 120
 QY 121 TGCAGAGCTTATGCTACCTTACACAGCTTGTGATGATGAGCTGGTGAAGAGGCT 180
 DB 121 TGCAGAGCTTATGCTACCTTACACAGCTTGTGATGATGAGCTGGTGAAGAGGCT 180
 QY 181 GGAAGAGCTTATGCTACCTTACACAGCTTGTGATGATGAGCTGGTGAAGAGGCT 240
 DB 181 GGAAGAGCTTATGCTACCTTACACAGCTTGTGATGATGAGCTGGTGAAGAGGCT 240
 QY 241 CAAATATTCAGAGGCAAGGCACTTGTGATGATGAGCTGGTGAAGAGGCT 300
 DB 241 GAGAGAGCTTCAAGAGGCAAGGCACTTGTGATGATGAGCTGGTGAAGAGGCT 300
 QY 301 CAGCTGAGAGCTTCAAGAGGCAAGGCACTTGTGATGATGAGCTGGTGAAGAGGCT 360
 DB 301 CAGCTGAGAGCTTCAAGAGGCAAGGCACTTGTGATGATGAGCTGGTGAAGAGGCT 360
 QY 361 GAGGAGAGGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 361 TACGATTAGCTA---CTTGTACTCTGGGGCAAGGCAAGGCAAGGCTCA 417

RESULT 7
 ID T05312 standard; DNA; 429 BP.
 AC T05312;
 DT 02-FEB-1996 (first entry)
 DE Mab SCH94.03 heavy chain DNA.
 KM Monoclonal antibody; Mab; SCH94.03; hybridoma; central nervous system;
 KM CNS; demyelination; multiple sclerosis; neural disease; therapeutic;
 OS ds.
 PN Mus sp.
 FH Key Location/Qualifiers
 FT cds 1..429
 FT signal_peptide 1..57
 FT mat_peptide 58..429
 FT /*tag= a
 FT /*tag= b
 FT /*tag= c
 PN W09530004-A1.
 PD 09-NOV-1995.
 PR 27-APR-1995; U05262.
 PR 29-APR-1994; US-236520.
 PA (MAYO-) MAYO FOUNDATION.
 PI Miller DJ, Rodriguez M;
 DR WPI: 95-393077/50.
 P-PSDB: R84554.
 PT Monoclonal antibodies which stimulate central nervous system
 PT re-myelination - are produced by hybridoma ATCC CRL 11627, for
 PT treating multiple sclerosis, and viral or post-neural diseases of
 PT the CNS.
 PS Disclosure: Page 38; 63pp: English.
 CC Hybridoma ATCC CRL 11627 was obtained from a SJL/J mouse injected with
 CC spinal cord homogenate from a mammal uninfected with any
 CC demyelinating disease. The hybridoma produced a monoclonal antibody
 CC (SCH94.03) useful in promoting CNS remyelination. The SCH94.03
 CC heavy chain germline sequence is given in T05312.
 SQ Sequence 429 BP: 109 A; 111 C; 113 G; 96 T;

CC antibody 4

FT	misc_feature	109.465
FT	misc_feature	466.499

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FT      /*tag- d
FT      /note- "constant region (encoded protein not given in...
FT      specification)"
PD      WO632495-A1.
PD      17-OCT-1996.
PD      06-APR-1996. KR0045.
PR      08-APR-1995; KR-008176.
PA      (GLDS ) LG CHEM LTD.
PI      Kang CY, Kim JG;
DR      WPI: 96-477145/47.
DR      P-RSDB: W04332.
PT      Monoclonal antibody specific for human 4-1BB - useful as
PT      immunospecific agent for treating autoimmune diseases and preventing
PT      organ transplant rejection.
PS      Claim 3; Fig 2a; 37p; English.
CC      T38509 and T38510 represent the coding sequences for the variable regions
CC      of the heavy and light chains of the antibody of the invention. The
CC      antibody of the invention (designated 4B4-1-1) is a monoclonal antibody
CC      (MAB) specific for human 4-1BB. 4-1BB encodes a member of the tumour
CC      necrosis factor receptor family of integral membrane proteins. 4-1BB is
CC      an accessory molecule expressed on the surface of T-cells in the initial
CC      stage of activation. The accessory molecules on the T-cell bind to the
CC      corresponding ligand on the antigen-presenting cell and this accelerates
CC      the activation of the T- and antigen-presenting cells, thereby promoting
CC      various immune responses. The MAB is specific for human 4-1BB, which is
CC      selectively expressed on activated T-cells. The MAB is useful as an
CC      immunosuppressive agent. It can be used for the treatment of autoimmune
CC      diseases, such as rheumatoid arthritis, and for preventing rejection...
SQ      Sequence 499 BP; 127 A; 135 C; 123 G; 114 T;

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Query Match      73.4%; Score 308.4; DB 1; Length 499;
Best Local Similarity 85.2%; Pred. No. 9.5e-78;
Matches 358; Conservative 0; Mismatches 56; Indels 6; Gaps 1;

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QY      1 ATGGGATGGAGCTATATCATCTCTTCTTGGTATCAACAGCTACAGTGTCCATCCAG 60
DB      ATGGGATGGAGCTATATCATCTCTTCTTGGTATCAACAGCTACAGTGTCCATCCAG 111
QY      61 GTCCAACTGGACGAGCTGTGGGCTGAGCTGTGAAGCTGTGAGCTGCTGAGCTGTGC 120
DB      GTCCAACTGGACGAGCTGTGGGCTGAGCTGTGAAGCTGTGAGCTGCTGAGCTGTGC 171
QY      121 TGCAGGCTATGCTACACCTTACACCTGATGATGATGATGATGATGATGATGATGATG 180
DB      TGCAGGCTATGCTACACCTTACACCTGATGATGATGATGATGATGATGATGATGATG 231
QY      181 GGACAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 240
DB      GGACAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 291
QY      241 CAAATATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB      CAAATATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 351
QY      301 CAGCTACAGAGCTGATCATCTGAGAGCTCTCGGCTACTATGATGATGATGATGATGATG 360
DB      CAGCTACAGAGCTGATCATCTGAGAGCTCTCGGCTACTATGATGATGATGATGATGATG 411
QY      352 CAATCTAGCAGAGCTGATCATCTGAGAGCTCTCGGCTACTATGATGATGATGATGATGATG 420
DB      CAATCTAGCAGAGCTGATCATCTGAGAGCTCTCGGCTACTATGATGATGATGATGATGATG 465
QY      412 ACGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 465
DB      ACGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG

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RESULT 10
ID      T36303 standard; cDNA: 433 BP.
AC      T36303;
DE      Anti-hepatitis B heavy chain variable region cDNA in pING2006E.
KW      Immunoglobulin G; IgG; heavy chain; recombinant production;
      antibody; passive immunisation; serum sickness; anaphylactic shock;

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KW      Immunoassay; imaging; reagent; complement mediated lysis;
KW      therapy; hepatitis B virus; variable region; mouse; HBV; ss.
OS      Mus spp.
FH      Key      Location/Qualifiers
FT      mat_peptide      26..433
FT      /*tag- a
PD      U5559589-A.
PD      21-JAN-1997.
PR      01-NOV-1985; 793980.
PR      29-MAR-1990; US-501092.
PR      01-NOV-1985; US-793980.
PR      27-OCT-1986; WO-002269.
PR      24-JUL-1987; US-077528.
PR      11-JAN-1988; US-142039.
PR      08-DEC-1992; US-987555.
PR      18-AUG-1994; US-299085.
PA      (XOMA ) XOMA CORP.
PI      Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI      Wall R, Wilcox GL;
DR      WPI: 97-107579/10.
DR      P-RSDB: W10584.
PT      Nucleic acid encoding immunoglobulin fragment - comprising
PT      di:clstronic transcription unit with pectate lyase signal sequences
PS      Example; Fig 1B; 95p; English.
CC      The present sequence is the anti-hepatitis B heavy chain variable
CC      region cDNA in pING2006E, which was used in the preparation of a
CC      novel polynucleotide molecule encoding an Ig fragment. The DNA
CC      molecule comprises 2 DNA sequences encoding 2 pectate lyase
CC      secretion signal sequences respectively linked to a DNA sequence
CC      encoding an Ig Fd molecule or Ig light chain, operably linked to a
CC      single prokaryotic promoter so as to form a di:clstronic
CC      transcription unit, provided that the Ig fragment can bind an
CC      antigen and is produced and secreted by an E. coli host cell when
CC      the nucleic acid molecule is expressed in the host cell.
CC      The polynucleotide molecule is used for the production of
CC      recombinant antibodies, which can be used for passive immunisation
CC      without negative immune reactions (e.g. serum sickness and
CC      anaphylactic shock), in labelled forms as immunoassay or imaging
CC      reagents, in complement mediated lysis and for therapeutic
CC      purposes when coupled to a toxin or other therapeutic agent.
SQ      Sequence 433 BP; 102 A; 126 C; 108 G; 97 T;

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Query Match      71.0%; Score 298; DB 1; Length 433;
Best Local Similarity 84.0%; Pred. No. 7.5e-75;
Matches 353; Conservative 0; Mismatches 55; Indels 12; Gaps 1;

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QY      1 ATGGGATGGAGCTATATCATCTCTTCTTGGTATCAACAGCTACAGTGTCCATCCAG 60
DB      ATGGGATGGAGCTATATCATCTCTTCTTGGTATCAACAGCTACAGTGTCCATCCAG 85
QY      26 ATGGGATGGAGCTATATCATCTCTTCTTGGTATCAACAGCTACAGTGTCCATCCAG 85
DB      ATGGGATGGAGCTATATCATCTCTTCTTGGTATCAACAGCTACAGTGTCCATCCAG 145
QY      61 GTCCAACTGGACGAGCTGTGGGCTGAGCTGTGAAGCTGTGAGCTGCTGAGCTGTGC 120
DB      GTCCAACTGGACGAGCTGTGGGCTGAGCTGTGAAGCTGTGAGCTGCTGAGCTGTGC 145
QY      121 TGCAGGCTATGCTACACCTTACACCTGATGATGATGATGATGATGATGATGATGATG 180
DB      TGCAGGCTATGCTACACCTTACACCTGATGATGATGATGATGATGATGATGATGATG 205
QY      146 TGCAGGCTATGCTACACCTTACACCTGATGATGATGATGATGATGATGATGATGATG 205
DB      TGCAGGCTATGCTACACCTTACACCTGATGATGATGATGATGATGATGATGATGATG 240
QY      181 GGACAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 240
DB      GGACAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 265
QY      206 GGACAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 265
DB      GGACAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300
QY      241 CAAATATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB      CAAATATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 325
QY      266 GAGAGTTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 325
DB      GAGAGTTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY      301 CAGCTACAGAGCTGATCATCTGAGAGCTCTCGGCTACTATGATGATGATGATGATGATG 360
DB      CAGCTACAGAGCTGATCATCTGAGAGCTCTCGGCTACTATGATGATGATGATGATGATG 385
QY      326 CAATCTAGCAGAGCTGATCATCTGAGAGCTCTCGGCTACTATGATGATGATGATGATGATG 385
DB      CAATCTAGCAGAGCTGATCATCTGAGAGCTCTCGGCTACTATGATGATGATGATGATGATG 420
QY      361 GAGGATGGAGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB      GAGGATGGAGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG

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Db 386 GACTGCT-----TTGCTTACTGGGCGCAAGGACTCTGCTACCGCTCTCTCA 433

RESULT 11

ID T36304 standard; cDNA; 420 BP.

AC T36304;

DT 21-OCT-1997 (first entry)

DE Anti-hepatitis B heavy chain variable region cDNA in pING2012E.

KM Immunoglobulin G; IgG; heavy chain; recombinant production;

KW antibody; passive immunisation; serum sickness; anaphylactic shock;

KM therapy; hepatitis B virus; variable region; HBV; ss.

OS Mus spp.

FN Key

FT mat_peptide 13.420

FT /*tag= a

PN US595898-A.

PD 21-JAN-1997.

PF 01-NOV-1985; 793980.

PR 29-MAR-1990; US-501092.

PR 01-NOV-1985; US-793980.

PR 27-OCT-1986; WO-002269.

PR 24-JUL-1987; US-077528.

PR 11-JAN-1988; US-142039.

PR 08-DEC-1992; US-987555.

PR 18-AUG-1994; US-299085.

PA (XOMA) XOMA CORP.

PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;

PI Wall R, Wilcox GL;

DR WPI: 97-107579/10.

DR P-SDB: W10584.

PT Nucleic acid encoding immunoglobulin fragment - comprising

PS dielctronic transcription unit with pectate lyase signal sequences

CC Example; Fig 12B; 98pp; English.

CC The present sequence is the anti-hepatitis B heavy chain variable

CC region cDNA in pING2012E, which was used in the preparation of a

CC novel polynucleotide molecule encoding an Ig fragment. The DNA

CC molecule comprises 2 DNA sequences encoding 2 pectate lyase

CC secretion signal sequences respectively linked to a DNA sequence

CC encoding an Ig Fd molecule or Ig light chain, operably linked to a

CC single prokaryotic promoter so as to form a dielctronic

CC transcription unit, provided that the Ig fragment can bind an

CC antigen and is produced and secreted by an E. coli host cell when

CC the nucleic acid molecule is expressed in the host cell.

CC The polynucleotide molecule is used for the production of

CC recombinant antibodies, which can be used for passive immunisation

CC without negative immune reactions (e.g. serum sickness and

CC anaphylactic shock). In labelled forms as immunoassay or imaging

CC reagents, in complement mediated lysis and for therapeutic

CC purposes when coupled to a toxin or other therapeutic agent.

SQ Sequence 420 BP; 102 A; 109 C; 110 G; 99 T;

Query Match 71.0%; Score 298; DB 1; Length 420;

Best Local Similarity 84.0%; Pred. No. 7.4e-75;

Matches 353; Conservative 0; Mismatches 55; Indels 12; Gaps 1;

QY 1 ATGGGATGAGCTGATATATCTCTCTTGGATGAACAGCTACAGGTCCATCCAG 60

DB 13 ATGGGATGAGCTGATATATCTCTCTTGGATGAACAGCTACAGGTCCATCCAG 72

QY 61 GTCCAACTGACAGAGCTGGGGCTGAGCTTGAAGCCTGGGACTGAGTGAAGTGC 120

DB 73 GTCCAACTGACAGAGCTGGGGCTGAGCTTGAAGCCTGGGACTGAGTGAAGTGC 132

QY 121 TGCAGGGTTATGGCTACACCTTCACAGCTACTGATGACATGGGGTGAAGAGGCT 180

DB 133 TGCAGGGCTTGGCTACACCTTCACAGCTACTGATGACATGGGGTGAAGAGGCT 192

QY 181 GGACAGGCTTGAAGTGAAGAGATGATCTCTTGAAGAGTAACTACTACTCAAT 240

DB 193 GGACAGGCTTGAAGTGAAGAGATGATCTCTTGAAGAGTAACTACTACTCAAT 252

QY 241 CAAAATTCAGAGGCGCAGCCACATTGACTGTAGACATTTCTCCAGCAGACCTACATG 300

DB 253 GAGAAGTTCAGAGGCGCAGCCACATTGACTGTAGACATTTCTCCAGCAGACCTACATG 312

QY 301 CAGCTCAGCAGCCTGACATCTGAGAGCTCTCGGCTCTACTTTGTGCAAGAGGGGTTAC 360

DB 313 CAGCTCAGCAGCCTGACATCTGAGAGCTCTCGGCTCTACTTTGTGCTTATGATATAC 372

QY 361 GAGGATGGGACTATGATGACTGAGGCTGAAGGCAAGCTCAGTACCGTCTCCCA 420

DB 373 GACTGCT-----TTGCTTACTGGGCGCAAGGACTCTGCTACCGCTCTCTCA 420

RESULT 12

ID V18553 standard; DNA; 420 BP.

AC V18553;

DT 05-JUN-1998 (first entry)

DE Human anti-hepatitis antibody heavy chain gene in pING2012E.

KM Mouse; murine; human anti-hepatitis antibody; heavy chain;

KW Immunoglobulin fragment production; Ig fragment production;

KW monoclonal antibody L6; human lung carcinoma cell;

OS Homo sapiens.

OS Synthetic.

FN Key

FT mat_peptide 13.433

FT /*tag= a

PN US5698435-A.

PD 16-DEC-1997.

PF 06-JUN-1995; 467140.

PR 29-MAR-1990; US-501092.

PR 01-NOV-1985; US-793980.

PR 27-OCT-1986; WO-002269.

PR 24-JUL-1987; US-077528.

PR 11-JAN-1988; US-142039.

PR 08-DEC-1992; US-987555.

PR 18-AUG-1994; US-299085.

PR 06-JUN-1995; US-467140.

PA (XOMA) XOMA CORP.

PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,

PI Wall R, Wilcox GL;

DR WPI: 98-051492/05.

DR P-SDB: W47510.

PT DNA encoding secretable immunoglobulin fragments - comprising at

PS least the variable regions of light or heavy chains

CC Example II; Fig 12B; 98pp; English.

CC The present sequence was used in the development of a novel method

CC for the production of an immunoglobulin (Ig) fragment capable of

CC binding an antigen. The method comprises culturing an E. coli host

CC that has been transformed with a nucleic acid molecule encoding the

CC Ig fragment, under conditions so that the Ig fragment is produced

CC and secreted. The nucleic acid molecule comprises DNA sequences

CC encoding: (a) pectate lyase secretion signal sequences operably

CC linked to a DNA sequence encoding at least the variable region of

CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence

CC operably linked to a DNA sequence encoding at least the variable

CC region of an Ig light chain, where (a) and (b) are operably linked

CC to a single prokaryotic promoter to form a dielctronic

CC transcription unit. The method is used to produce chimeric Fab

CC molecules, e.g. derived from murine monoclonal antibody L6 raised

CC against human lung carcinoma cells. The invention provides a novel

CC approach for producing genetically engineered antibodies of

CC desired variable region specificity and constant region

CC properties. The cloned Ig gene products can be produced by

CC expression in genetically engineered organisms. The application of

CC chemical gene synthesis, recombinant DNA cloning and production of

CC specific Ig chains in various organisms provides an effective

CC solution for the efficient large scale production of human

CC monoclonal antibodies. The invention also provides a solution to

CC the problem of class switching antibody molecules.

SQ Sequence 420 BP; 102 A; 109 C; 110 G; 99 T;

Query Match 71.0%; Score 298; DB 1; Length 420;
 Best Local Similarity 84.0%; Pred. No. 7.4e-75;
 Matches 353; Conservative 0; Mismatches 55; Indels 12; Gaps 1;

QY 1 ATGGATGAGCTGATATCTCTCTTGTATCAACAGCTACAGTGTCCATCCAG 60
 DB 13 ATGGATGAGCTATATATCTCTCTTGTATCAACAGCTACAGTGTCCATCCAG 72
 QY 61 GTCCACATGACAGCTGAGGCTGAGCTTGAAGCCGAGGCTTCAAGTGAAGCTTC 120
 DB 73 GTCCACATGACAGCTGAGGCTGAGCTTGAAGCCGAGGCTTCAAGTGAAGCTTC 132
 QY 121 TGCAGAGGTTATGCTTACACCTTTCACAGCTACAGTGTCCATCCAGAGGCT 180
 DB 133 TGCAGAGGCTTGTGCTTACACCTTTCACAGCTACAGTGTCCATCCAGAGGCT 192
 QY 161 GGACAAAGGCTTGTGCTTACAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 240
 DB 193 GGACAAAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 252
 QY 241 CAAATATTCAGAGGCTGAGGCTGAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 300
 DB 253 CAAATATTCAGAGGCTGAGGCTGAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 312
 QY 301 CAGCTCAGCAGCTGATCATCTGAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 360
 DB 313 CAGCTCAGCAGCTGATCATCTGAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 372
 QY 361 GACGATGAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 420
 DB 373 GACTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 420

RESULT 13
 V18554 standard; DNA: 433 BP.
 AC V18554:
 DT 05-JUN-1998 (first entry)
 DE Human anti-hepatitis antibody heavy chain gene in PING2006E.
 KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
 KW Immunoglobulin fragment production; Ig fragment production;
 KW monoclonal antibody L6; human lung carcinoma cell;
 KW PING2006E; ss.
 OS Homo sapiens.
 OS Synthetic.
 FH Key
 FT mat_peptide Location/Qualifiers
 FT 26..433
 FT /*tag= a

US5698435-A.
 PD 16-DEC-1997. 467140.
 PF 06-JUN-1995; US-501092.
 PR 29-MAR-1980; US-793980.
 PR 01-NOV-1985; US-793980.
 PR 27-OCT-1986; WO-002269.
 PR 24-JUL-1987; US-077528.
 PR 11-JAN-1988; US-142039.
 PR 08-DEC-1992; US-987555.
 PR 18-AUG-1994; US-299085.
 PR 06-JUN-1995; US-467140.
 PA (XOMA) XOMA CORP.
 PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
 PI Wall R, Wilcox GL,
 DR WPI: 98-051492/05.
 DR P-PSDB: W47510.
 PT DNA encoding secretable immunoglobulin fragments - comprising at
 PT least the variable regions of light or heavy chains
 PS Example II; Fig 12B; 98PP; English.
 CC The present sequence was used in the development of a novel method
 CC for the production of an immunoglobulin (Ig) fragment capable of
 CC binding an antigen. The method comprises culturing an E. coli host
 CC that has been transformed with a nucleic acid molecule encoding the

CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. The nucleic acid molecule comprises DNA sequences
 CC encoding: (a) pectate lyase secretion signal sequence operably
 CC linked to a DNA sequence encoding at least the variable region of
 CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
 CC operably linked to a DNA sequence encoding at least the variable
 CC region of an Ig light chain, where (a) and (b) are operably linked
 CC to a single prokaryotic promoter to form a dicistronic
 CC transcription unit. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody L6 raised
 CC against human lung carcinoma cells. The invention provides a novel
 CC approach for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region
 CC properties. The cloned Ig gene products can be produced by
 CC expression in genetically engineered organisms. The application of
 CC chemical gene synthesis, recombinant DNA cloning and production of
 CC specific Ig chains in various organisms provides an effective
 CC solution for the efficient large scale production of human
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.
 CC Sequence 433 BP; 102 A; 126 C; 108 G; 97 T;

Query Match 71.0%; Score 298; DB 1; Length 433;
 Best Local Similarity 84.0%; Pred. No. 7.5e-75;
 Matches 353; Conservative 0; Mismatches 55; Indels 12; Gaps 1;

QY 1 ATGGATGAGCTGATATCTCTCTTGTATCAACAGCTACAGTGTCCATCCAG 60
 DB 26 ATGGATGAGCTATATATCTCTCTTGTATCAACAGCTACAGTGTCCATCCAG 85
 QY 61 GTCCAAATGACAGGCTGAGGCTGAGCTTGTGAAGCCTGGAGCTTCAAGTGTCC 120
 DB 86 GTCCAAATGACAGGCTGAGGCTGAGCTTGTGAAGCCTGGAGCTTCAAGTGTCC 145
 QY 121 TGCAGAGGTTATGCTTACACCTTTCACAGCTACAGTGTCCATCCAGAGGCT 180
 DB 146 TGCAGAGGCTTGTGCTTACACCTTTCACAGCTACAGTGTCCATCCAGAGGCT 205
 QY 181 GGACAAAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 240
 DB 206 GGACAAAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 265
 QY 241 CAAATATTCAGAGGCTGAGGCTGAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 300
 DB 266 GAGAAATTCAGAGGCTGAGGCTGAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 325
 QY 301 CAGCTCAGCAGCTGATCATCTGAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 360
 DB 326 CAGCTCAGCAGCTGATCATCTGAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 385
 QY 361 GACGATGAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 420
 DB 386 GACTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 433

RESULT 14
 V03866 standard; DNA: 433 BP.
 ID V03866:
 DT 01-JUN-1998 (first entry)
 DE Human anti-hepatitis antibody heavy chain gene in PING2006E.
 KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
 KW Immunoglobulin fragment production; Ig fragment production;
 KW monoclonal antibody L6; human lung carcinoma cell;
 KW PING2006E; ss.
 OS Homo sapiens.
 OS Synthetic.
 FH Key
 FT mat_peptide Location/Qualifiers
 FT 26..433
 FT /*tag= a

US5693493-A.
 PD 02-DEC-1997.

PF 25-MAY-1995; 450731.
 PR 29-MAR-1990; US-501092.
 PR 01-NOV-1985; US-793980.
 PR 27-OCT-1986; WO-002269.
 PR 24-JUL-1987; US-077528.
 PR 11-JAN-1988; US-142039.
 PR 08-DEC-1992; US-987555.
 PR 18-AUG-1994; US-299085.
 PR 25-MAY-1995; US-450731.
 PA (XOMA) XOMA CORP.
 PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
 PI Wall R, Wilcox GL.
 DR WPI: 98-031749/03.
 DR P-PSDB: W41054.
 PT Production of chimeric antibody fragments - by culturing E. coli
 PT transformed with dicistronic expression cassette
 PS Example II; Fig 12B; 98pp; English.
 CC The present sequence was used in the development of a novel method
 CC for the production of an immunoglobulin (Ig) fragment capable of
 CC binding an antigen. The method comprises culturing an E. coli host
 CC that has been transformed with a nucleic acid molecule encoding the
 CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. The nucleic acid molecule comprises DNA sequences
 CC encoding: (a) pectate lyase secretion signal sequence operably
 CC linked to a DNA sequence encoding at least the variable region of
 CC an Ig molecule; and (b) pectate lyase secretion signal sequence
 CC operably linked to a DNA sequence encoding at least the variable
 CC region of an Ig light chain, where (a) and (b) are operably linked
 CC to a single prokaryotic promoter to form a dicistronic
 CC transcription unit. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody L6 raised
 CC against human lung carcinoma cells. The invention provides a novel
 CC approach for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region
 CC properties. The cloned Ig gene products can be produced by
 CC expression in genetically engineered organisms. The application of
 CC chemical gene synthesis, recombinant DNA cloning and production of
 CC specific Ig chains in various organisms provides an effective
 CC solution for the efficient large scale production of human
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.
 SQ Sequence 433 BP; 102 A; 126 C; 108 G; 97 T;

Query Match 71.0%; Score 298; DB 1; Length 433;
 Best Local Similarity 84.0%; Pred. No. 7.5e-75;
 Matches 353; Conservative 0; Mismatches 55; Indels 12; Gaps 1;

QY 1 ATGGATGAGCTGTATCATCTCTTCTTGTGATCAACAGCTACAGTGTCCACG 60
 DB 26 ATGGATGAGCTGTATCATCTCTTCTTGTGATCAACAGCTACAGTGTCCACG 85
 QY 61 GTCCAACTGACAGAGCTGGGGCTGAGCTGTGAAAGCTTGGAGTGTCC 120
 DB 86 GTCCAACTGACAGAGCTGGGGCTGAGCTGTGAAAGCTTGGAGTGTCC 145
 QY 121 TGCAGAGGTATGCTACACCTTCCACAGCTAGTGTGAGTGGGAGAGAGGCT 180
 DB 146 TGCAGAGGTATGCTACACCTTCCACAGCTAGTGTGAGTGGGAGAGGCT 205
 QY 181 GGACAAAGGCTTGTAGTGTGAGAGATGATCTTCTGAGATATTAATACTAAT 240
 DB 206 GGACAAAGGCTTGTAGTGTGAGAGATGATCTTCTGAGATATTAATAAT 265
 QY 241 CAAAATTCAGAGGCAAGGCCACATTGATGTAGACATTTCTCCACAGCCTACATG 300
 DB 266 GAAAGATTCAGAGGCAAGGCCACATTGATGTAGACATTTCTCCACAGCCTACATG 325
 QY 301 CAGCTGACAGCCTGACATCTGAGAGTCTGGGCTACTATGTGTGAAGGGGGTAC 360
 DB 326 CAGCTGACAGCCTGACATCTGAGAGTCTGGGCTACTATGTGTGAAGGGGGTAC 385
 QY 361 GAGGATGGAGTATGCTATGACTACTGGGGTCAAGGACCTCAGTCCACTCTCTCA 420

DB 386 GACTGCT-----TTGCTTACTGGGGCAAGGAGACTGTGTCACCGTCTCTCA 433

RESULT 15
 V03836
 ID V03836 standard; DNA; 420 BP.
 AC V03836;
 DT 01-JUN-1998 (first entry)
 DE Human anti-hepatitis antibody heavy chain gene in pING2012E.
 KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
 KW Immunoglobulin fragment production; Ig fragment production;
 KW monoclonal antibody L6; human lung carcinoma cell;
 KW pING2012E; ss.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT mat_peptide 13..433
 FT /tag= a
 FT US5693493-A.
 PD 02-DEC-1997.
 PF 25-MAY-1995; 450731.
 PR 29-MAR-1990; US-501092.
 PR 01-NOV-1985; US-793980.
 PR 27-OCT-1986; WO-002269.
 PR 24-JUL-1987; US-077528.
 PR 11-JAN-1988; US-142039.
 PR 08-DEC-1992; US-987555.
 PR 18-AUG-1994; US-299085.
 PR 25-MAY-1995; US-450731.
 PA (XOMA) XOMA CORP.
 PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
 PI Wall R, Wilcox GL.
 DR WPI: 98-031749/03.
 DR P-PSDB: W41054.
 PT Production of chimeric antibody fragments - by culturing E. coli
 PT transformed with dicistronic expression cassette
 PS Example II; Fig 12B; 98pp; English.
 CC The present sequence was used in the development of a novel method
 CC for the production of an immunoglobulin (Ig) fragment capable of
 CC binding an antigen. The method comprises culturing an E. coli host
 CC that has been transformed with a nucleic acid molecule encoding the
 CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. The nucleic acid molecule comprises DNA sequences
 CC encoding: (a) pectate lyase secretion signal sequence operably
 CC linked to a DNA sequence encoding at least the variable region of
 CC an Ig molecule; and (b) pectate lyase secretion signal sequence
 CC operably linked to a DNA sequence encoding at least the variable
 CC region of an Ig light chain, where (a) and (b) are operably linked
 CC to a single prokaryotic promoter to form a dicistronic
 CC transcription unit. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody L6 raised
 CC against human lung carcinoma cells. The invention provides a novel
 CC approach for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region
 CC properties. The cloned Ig gene products can be produced by
 CC expression in genetically engineered organisms. The application of
 CC chemical gene synthesis, recombinant DNA cloning and production of
 CC specific Ig chains in various organisms provides an effective
 CC solution for the efficient large scale production of human
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.
 SQ Sequence 420 BP; 102 A; 109 C; 110 G; 99 T;

Query Match 71.0%; Score 298; DB 1; Length 420;
 Best Local Similarity 84.0%; Pred. No. 7.4e-75;
 Matches 353; Conservative 0; Mismatches 55; Indels 12; Gaps 1;

QY 1 ATGGATGAGCTGTATCATCTCTTCTTGTGATCAACAGTGTCCACG 60
 DB 13 ATGGATGAGCTGTATCATCTCTTCTTGTGATCAACAGTGTCCACG 72

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OY 61 GTCCAACTGCAGACGCTGGGGCTGAGCTGTGAAGCCTGGGACTTCAGTGAAGCTGTCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 73 GTCCAAATTGCAGACGCTGGGGCTGAACCTGGGGCTTCAGTGAAGTGTCC 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 TGCAGGGTTATGGCTACACCTTCACCGACTACTGATGCACTGGGTGAACAGAGGCT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 133 TGCAGGGCTCTGGCTACACCTTCACCGACTACTGATGCACTGGGTGAACAGAGGCT 192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 GGACAAAGGCTTGAAGTGGAGAGATGATCCTCTGAGAGTAAATACTACTACAT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 193 GGACAAAGGCTTGAAGTGGAGAGATGATCCTCTGAGAGTAAATACTACTACAT 252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 241 CAAAAATTCAAGGGCAAGGCCACATTTGACTGTAGACATTTCTCCAGCACAGCCTACATG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 253 GAGAAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAATCTCCAGCACAGCCTACATG 312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 301 CAGCTCAGACGCTGACATCTGAGAGACTCTGGCTCTACTATTTGCAAGAGGGGTTAC 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 313 CAAGCTCAGACGCTGACATCTGAGAGACTCTGGCTCTACTATTTGCAAGAGGGGTTAC 372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 361 GACGGATGGGACTATGCTATTGACTACTGGGGTCAAGGACCTCAGTCACCGTCTCTCA 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 373 GACTGGT-----TTGCTTACTGGGGCCAAAGGACTCTGTGTCACCGTCTCTCA 420
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Search completed: May 11, 1999, 12:03:29
Job time: 1536 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:23:24 ; Search time 30.48 Seconds
(without alignments)
172.062 Million cell updates/sec

Title: US-08-700-737-15

Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHSQ.....DGMVDYIDYWGQTSVTSS 140

Scoring table: BLOSUM62

Searched: 116738 seqs, 37460341 residues

Database : PIR-58:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	603	79.7	138	2 E32513	Ig heavy chain pre
2	599.5	79.2	139	1 MHMS18	Ig heavy chain pre
3	592.5	78.3	141	2 JLU0076	Ig heavy chain pre
4	579.5	76.6	135	2 A30577	Ig heavy chain pre
5	576	76.1	131	2 A27472	Ig heavy chain pre
6	559	73.8	138	1 HVMST7	Ig heavy chain pre
7	556	73.4	117	1 HVMST02	Ig heavy chain pre
8	555	73.3	136	2 B47159	Ig heavy chain pre
9	554.5	73.2	137	1 GZMS43	Ig heavy chain pre
10	552	72.9	136	2 PL0208	Ig heavy chain pre
11	551.5	72.9	137	2 E29380	Ig heavy chain pre
12	551.5	72.9	137	2 E29380	Ig heavy chain pre
13	546.5	72.2	136	2 JLU0077	Ig heavy chain pre
14	543	71.7	117	1 HVMST3	Ig heavy chain pre
15	537	70.9	117	1 HVMST61	Ig heavy chain pre
16	533.5	70.5	120	2 B22769	Ig heavy chain pre
17	533	70.4	140	2 PH1482	Ig heavy chain pre
18	532	70.3	140	2 HVMST7	Ig heavy chain pre
19	529.5	69.9	139	2 PS0024	Ig heavy chain pre
20	527.5	69.7	120	2 S41394	Ig heavy chain pre
21	527	69.6	117	1 HVMST3	Ig heavy chain pre
22	525	69.4	117	1 MHMSB4	Ig heavy chain pre
23	524	69.2	138	2 S21810	Ig heavy chain pre
24	523	69.1	116	2 S21810	Ig heavy chain pre
25	520	68.7	140	2 PH1489	Ig heavy chain pre
26	519.5	68.6	116	2 S33751	Ig heavy chain pre
27	519	68.6	117	1 HVMST5	Ig heavy chain pre
28	518.5	68.5	139	2 A27609	Ig heavy chain pre
29	517.5	68.4	139	2 A39276	Ig heavy chain pre
30	517	68.3	140	2 PH1484	Ig heavy chain pre
31	515	68.0	123	2 S20646	Ig heavy chain pre
32	514.5	68.0	287	3 PC4402	Ig heavy chain pre
33	514	67.9	120	2 S25175	Ig heavy chain pre
34	511	67.5	140	2 PH1488	Ig heavy chain pre
35	509.5	67.3	137	2 H32513	Ig heavy chain pre
36	507	67.0	135	2 PH1493	Ig heavy chain pre
37	507	67.0	122	2 S20643	Ig heavy chain pre
38	506	66.8	140	2 PH1486	Ig heavy chain pre
39	506	66.8	140	2 PH1498	Ig heavy chain pre

40 505.5 66.8 469 2 S37483 Ig gamma-2a chain
41 504.5 66.6 150 2 PN0444 Ig heavy chain v r
42 503 66.4 140 2 A36194 Ig heavy chain v r
43 503 66.4 135 2 PH1492 Ig heavy chain v r
44 502.5 66.4 126 2 S31930 Ig gamma chain pre
45 500 66.1 140 2 S04575 Ig heavy chain pre

ALIGNMENTS

RESULT 1
E32513
Ig heavy chain precursor V region (MRL22) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 20-Mar-1998
C:Accession: E32513
R:Kottler, R.; Stroh, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization a
A:Reference number: A94689; MUID:88331394
A:Accession: E32513
A:Molecule type: DNA
A:Residues: 1-138 <KOR>
A:Cross-References: GB:M20835; NID:9196945; PID:9196946
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 603; DB 2; Length 138;
Best Local Similarity 82.9%; Pred. No. 2.7e-45;
Matches 116; Conservative 7; Mismatches 15; Indels 2; Gaps 1;

QY 1 MGWSCIILFLVSTATSVHSQVQLQPGAFYVPRGTSVKLSCKGYCTFTSYMMHWKORP 60
Db 1 MGWSCIILFLVAAATGVHSQVQLQPGAFYVPRGASVSKLSCKASGYCTFTSYMMHWKORP 60
QY 61 GQGLEWIGEIDSESNNTNOKFKATLVDPISSTAYVMQSLSEDSAVYCCARGY 120
Db 61 GQGLEWIGNITPESSSTNNNEKFKATLVDPISSTAYVMQSLSEDSAVYCCARLY 120
QY 121 DGMVDYIDYWGQTSVTSS 140
Db 121 R-YAMVDYWGQTSVTSS 138

RESULT 2
MHMS18
Ig heavy chain precursor V region (B1-8) - mouse
N:Contains: Ig heavy chain precursor V region 186-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1992 #text_change 20-Mar-1998
C:Accession: A90809; B90809; A22769; A02034; A02036
R:Bothwell, A.L.M.; Paskind, M.; Reith, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies:
A:Reference number: A90809; MUID:81234548
A:Accession: A90809
A:Molecule type: DNA
A:Residues: 1-139 <B18>
A:Cross-References: GB:J00529; NID:9195114; PID:9195115
A:Accession: B90809
A:Molecule type: DNA
A:Residues: 1-117 <1862>
A:Note: The B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the h
A:Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA
R:Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination betwe
A:Reference number: A90971; MUID:84236026
A:Accession: A22769
A:Molecule type: protein

A:Residues: 20-139 <DII>
 A:Note: the V region of the BI-8 delta chain, derived as a spontaneous class:svt1ch var1
 of the mu chain
 C:Genetics:
 A:introns: 16/1
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-19/Delta: signal sequence #status predicted <SIG>
 F:20-139/Product: Ig kappa chain V region (BI-8) #status experimental <MAT>
 F:34-117/Delta: immunoglobulin homology <IMM>
 F:118-124/Region: D segment
 F:125-139/Region: J segment (JH2)

Query Match 79.2%; Score 599.5; DB 1; Length 139;
 Best Local Similarity 80.7%; Pred. No. 5.4e-45;
 Matches 113; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 DB 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 QY 61 GGGLEWIGIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDSAYVYCARGGY 120
 DB 61 GGGLEWIGIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDSAYVYCARGGY 120
 QY 121 DGMWDYAIIDYWGQGTSTVSS 140
 DB 121 YGSSY-FDYWGQGTTLTVSS 139

RESULT 3

Ig heavy chain precursor V region (anti-phenylloxazolone, 18C10) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998
 C:Accession: J10076
 R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
 M.Ol. Immunol. 25, 859-865, 1988
 A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reactive
 A:Reference number: J10076; MUID:89096973
 A:Accession: J10076

A:Molecule type: mRNA
 A:Residues: 1-141 <KAA>
 A:Cross-references: GB:M27788; NID:9195851; PID:9195852
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-19/Delta: signal sequence #status predicted <SIG>
 F:20-141/Product: Ig heavy chain #status predicted <MAT>
 F:34-117/Delta: immunoglobulin homology <IMM>
 F:50-94/Region: complementarity-determining 1
 F:69-85/Region: complementarity-determining 2
 F:123-135/Region: J2 segment
 F:136-141/Region: C

Query Match 78.3%; Score 592.5; DB 2; Length 141;
 Best Local Similarity 80.0%; Pred. No. 2.2e-44;
 Matches 112; Conservative 7; Mismatches 16; Indels 5; Gaps 1;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 DB 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 QY 61 GGGLEWIGIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDSAYVYCARGGY 120
 DB 61 GGGLEWIGIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDSAYVYCARGGY 120
 QY 121 DGMWDYAIIDYWGQGTSTVSS 140
 DB 121 AG-----DYWGQGTTLTVSS 135

RESULT 4
 Ig heavy chain precursor V region (MRL10) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
 C:Accession: A30577
 R:Koller, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Th
 J. Exp. Med. 161, 805-815, 1985
 A:Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r
 A:Reference number: A30577; MUID:85159423
 A:Accession: A30577
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <KOF>
 A:Cross-references: GB:M37621
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-117/Delta: immunoglobulin homology <IMM>

Query Match 76.6%; Score 579.5; DB 2; Length 135;
 Best Local Similarity 78.9%; Pred. No. 2.7e-43;
 Matches 112; Conservative 8; Mismatches 13; Indels 9; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 DB 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 QY 61 GGGLEWIGIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDSAYVYCAR--G 118
 DB 61 GGGLEWIGIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDSAYVYCARLWG 120
 QY 119 GYDGMWDYAIIDYWGQGTSTVSS 140
 DB 121 GF-----AYWGQGTTLTVSSA 135

RESULT 5

Ig heavy chain precursor V region (1E9) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 18-Oct-1996
 C:Accession: A27472
 R:Lin, A.Y.; Mack, P.W.; Champion, C.I.; Robinson, R.R.
 Gene 54, 33-40, 1987
 A:Title: Expression of mouse: human immunoglobulin heavy-chain cDNA in lymphoid cells
 A:Reference number: A27472; MUID:87277430
 A:Accession: A27472

A:Molecule type: mRNA
 A:Residues: 1-131 <LID>
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-19/Delta: signal sequence #status predicted <SIG>
 F:5-54/Region: complementarity-determining 1
 F:20-131/Product: Ig heavy chain V region 1E9 #status predicted <MAT>
 F:34-117/Delta: immunoglobulin homology <IMM>
 F:69-85/Region: complementarity-determining 2
 F:118-125/Region: complementarity-determining 3

Query Match 76.1%; Score 576; DB 2; Length 131;
 Best Local Similarity 82.8%; Pred. No. 5.3e-43;
 Matches 111; Conservative 4; Mismatches 15; Indels 4; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 DB 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 QY 61 GGGLEWIGIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDSAYVYCARGGY 120
 DB 61 GGGLEWIGIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDSAYVYCARGGY 120
 QY 121 DGMWDYAIIDYWGQGT 134

Db 121 D-W---FAFMGQGT 130

RESULT 6

HVMST7

Ig heavy chain precursor V region (TEPC 1017) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 30-May-1997

C:Accession: A02033

R:Gilliam, A.C.; Shen, A.; Richards, J.E.; Blattner, F.R.; Moshinski, J.F.; Tucker, P.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 4164-4168, 1984

A:Title: Illegitimate recombination generates a class switch from C-mu to C-delta in an

A:Reference number: A02033; MUID:84248078

A:Accession: A02033

A:Molecule type: mRNA

A:Residues: 1-138 <GTL>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-138/Product: Ig heavy chain V region (TEPC 1017) #status predicted <MAT>

F:34-117/Domain: V segment

F:118-123/Region: D segment

F:124-138/Region: J segment

Query Match

73.8%; Score 559; DB 1; Length 138;

Best Local Similarity 75.9%; Pred. No. 1,6e-41;

Matches 107; Conservative 12; Mismatches 18; Indels 4; Gaps 2;

Db 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSVKLSCKGYGFTSTYMMHWKORP 60

1 MGWSCIILFLVATATDVHSQVLOQPGAEIVKPGASVQLSCASGHTFTTYMMHWKORP 60

QY 61 GGGLEWIGEDIPSSNNYNNKFKGKATLTVDISSSTAYMOLSLTSEDSAVYTCARG-G 119

61 GGGLEWIGEDIPSSNNYNNKFKGKATLTVDISSSTAYMOLSLTSEDSAVYTCARG-G 120

QY 120 YDGMIDYADYMGQSTVYSS 140

Db 121 YDGMIDYADYMGQSTVYSS 138

RESULT 7

HVM502

Ig heavy chain precursor V region (102) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 23-Aug-1996

C:Accession: A02032

R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.

Cell 24, 625-637, 1981

A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som

A:Reference number: A90809; MUID:81234548

A:Accession: A02032

A:Molecule type: DNA

A:Residues: 1-117 <BOT>

A:Note: the sequence was determined from the germline gene

A:Note: the germline gene, cloned from a library of strain C57BL/6 DNA, is one of a set

1 (NPb antibodies)

C:Genetics:

A:Intons: 16/1

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (102) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match

73.4%; Score 556; DB 1; Length 117;

Best Local Similarity 89.7%; Pred. No. 2.4e-41;

Matches 104; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSVKLSCKGYGFTSTYMMHWKORP 60

1 MGWSCIILFLVATATDVHSQVLOQPGAEIVKPGASVQLSCASGHTFTTYMMHWKORP 60

QY 61 GGGLEWIGEDIPSSNNYNNKFKGKATLTVDISSSTAYMOLSLTSEDSAVYTCARG 116

61 GGGLEWIGEDIPSSNNYNNKFKGKATLTVDISSSTAYMOLSLTSEDSAVYTCARG 116

RESULT 8

B47159

Ig heavy chain V region, anti-carcinoma embryonic mald 184.66 antigen monoclonal anti-1d

C:Species: Mus musculus (house mouse)

C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996

C:Accession: B47159

R:Galda, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wengner, C.; Neumaier, M.

J. Biol. Chem. 268, 14138-14145, 1993

A:Title: Molecular characterization of a cloned idiotype cascade containing a networ

A:Reference number: A47159; MUID:93300804

A:Accession: B47159

A:Molecule type: DNA; protein

A:Residues: 1-136 <GAL>

A:Experimental source: hybridoma 6G6.C4

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:134421, NCBI:134422)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match

73.3%; Score 555; DB 2; Length 136;

Best Local Similarity 75.7%; Pred. No. 3.5e-41;

Matches 106; Conservative 12; Mismatches 18; Indels 4; Gaps 1;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSVKLSCKGYGFTSTYMMHWKORP 60

1 MGWSCIILFLVATATDVHSQVLOQPGAEIVKPGASVQLSCASGHTFTTYMMHWKORP 60

QY 61 GGGLEWIGEDIPSSNNYNNKFKGKATLTVDISSSTAYMOLSLTSEDSAVYTCARG 120

61 GGGLEWIGEDIPSSNNYNNKFKGKATLTVDISSSTAYMOLSLTSEDSAVYTCARG 120

QY 121 DGMIDYADYMGQSTVYSS 140

Db 121 GNR----DYMGQSTVYSS 136

RESULT 9

G2MS43

Ig heavy chain precursor V region (543) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 20-Mar-1998

C:Accession: A02038

R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore

Cell 24, 625-637, 1981

A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies:

A:Reference number: A90809; MUID:81234548

A:Accession: A02038

A:Molecule type: mRNA

A:Residues: 1-137 <BOT>

A:Cross-references: GB:J00539; NID:q195118; PID:q195119

A:Note: the gamma-2a chain mRNA was cloned from a hybridoma making antibodies to the

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-137/Product: Ig heavy chain V region (543) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:118-122/Region: D segment

F:123-137/Region: J segment (JH2)

Query Match

73.2%; Score 554.5; DB 1; Length 137;

Best Local Similarity	74.18;	Pred. NO.	3.9e-41;
Matches	106;	Conservative	9;
		Mismatches	19;
		Indels	9;
		Gaps	2;

```

QY 1 MGWSCIIFLIVSTATSVASVOVLOOPGAEILYKPGTSYKSCKGXGYFTSTYMHVQRP 60
Db 1 MGWSCIIFLFLATATGVASVOVLOOPGAEILYKPGASVKLSCSKASGYFTSTYMHVQRP 60
QY 61 GQGLEWIGEIDPESSENTYNOFKGKATLFLVDISSSTAYMQLSSLTSEDSAVYYCAR -- 118
Db 61 GRLGLEWICRIDPNSGGTYINNEHFSKATLTIDKESSTAYMQLSSLTSEDSAVYYCAR YRL 120
QY 118 GGYDGMWDYAIDYWGQGSIVTVSS 140
Db 121 GRV-----FDYWGCGTTLTVSS 137

```

RESULT 10
P10208

```

C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998
C:Accession: PI02208
R:Soucchon, H., Doyen, N., Riottot, M.M., Rougeon, F., Poljak, R.J.
Mol. Immunol. 27, 429-433, 1990
A:Title: Nucleotide sequence of the VH, VL regions of an anti-idiotopic antibody reacting with a myeloma cell
A:Reference number: PI0207
A:Accession: PI0208
A:Molecule type: mRNA
A:Residues: 1-136 <SOU>
A:Experimental source: hybridoma cell E225
C:Superfamily: Immunoglobulin V region; immunoglobulin homology...
F:1-19/Domain: signal sequence #status predicted <SIG>
F:34-117/Domain: immunoglobulin homology <IM>
F:50-54/Region: complementarity-determining 1
F:69-85/Region: complementarity-determining 2
F:118-125/Region: complementarity-determining 3
F:118-121/Region: D region
F:122-136/Region: JH region

```

Query Match	72.98;	Score 552;	DB 2;	Length 136;
Best Local Similarity	73.68;	Pred. No. 6.3e-41;		
Matches 103;	Conservative 15;	Mismatches 18;	Indels 4;	Gaps 1

[illegible]

```

RESULT 11
E29380
1g heavy chain precursor V region (AC-1001) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revission 31-Dec-1988 #text_change 20-Mar-1998
C:Accession: E29380
R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 1579-13583, 1987
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A:Reference: number: A2612; MUID:88007582
A:Accession: E29380
A:Molecule type: mRNA
A:Residues: 1-137 <CHE>
A:Cross-References: GB:M17164; GB:J02815; NID:G195411; PID:G195412
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

```

F;34-117/Domain: Immunoglobulin homology <IMM>

	Query Match	72.9%	Score 551.5;	DB 2;	Length 137;
	Best Local Similarity	77.9%	Pred. No. 7e-41;		
	Matches	109;	Conservative	8;	Mismatches 20; Indels 3; Gaps
OY	1	MGWSCIIIFLVSTATSVHSQVLOQPGEALVPCTSVKLSCKRGYGIFTSTWMAHWKORP	60		
Db	1	MGWSIIIFLVTATGAVSHSQVOLQOPGAELVPCTPSVSLCSKAGSYNETTSWIIMVKLRP	60		
OY	61	GQGLEMIDEPSEBENTNKKFKGKATLTVDISSPTAYMOLSSILTSDSNAVYYCARGCY	120		
Db	61	GQGLEMIWDITPGSGIINYNKKFKSKALTVDISSTAYMOLSSLASDSALTYCA-GQY	117		
OY	121	DGMDFAIIDMGQGSFTVVSS	140		
	:				
Db	120	GNLMFA--YWGCGILTIVTSA	137		

RESULT	12
F29380	

Ig heavy chain precursor V region (A003 40/567) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1998 #sequence_revision 31-Dec-1988 #text_change 20-Mar-1998
 C:Accession: F29380
 R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
 J. Biol. Chem. 262, 13579-13583, 1987
 A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
 A:Reference number: A92612; MUID:88007582
 A:Accession: F29380
 A:Molecule type: mRNA
 A:Residues: 1-137 <GB>
 A:Cross-references: GB:MI7165; GB:J02815; NID:g195409; PID:g195410
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IM>

Query Match	72.9%;	Score 551.5;	DB 2;	Length 137;
Best Local Similarity	75.0%;	Pred. No. 7e-41;		
Matches 105;	Conservative 12;	Mismatches 20;	Indels 3;	Gaps 1;

[illegible]

RESULT 13
 JI0077
 Ig heavy chain precursor V region (anti-phenylloxazalone, 6F6) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998
 C:Accession: JI0077
 R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
 MOL. Immunol. 25, 859-865, 1988
 A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross
 A:Reference number: JI0076, MUID:89069573
 A:Accession: JI0077
 A:Molecule type: mRNA
 A:Residues: 1-136 <KAA>
 A:Cross-references: GB:M27789; NID:g195853; PID:g195854
 A:Note: the authors translated the codon AGC for residue 114 as Arg
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>
 E:17-136/Product: Ig heavy chain #status predicted <MAT>
 F:31-114/Domain: immunoglobulin homology <IMM>
 F:47-51/Region: complementarity-determining 1
 F:66-82/Region: complementarity-determining 2
 F:118-130/Region: J2 segment
 F:131-136/Region: C

Query Match 72.2%; Score 546.5; DB 1; Length 136;
 Best Local Similarity 77.4%; Pred. No. 1.9e-40;
 Matches 106; Conservative 7; Mismatches 17; Indels 7; Gaps 2;
 QY 4 SCILFLVSTATSVHSQVQLQPGAEIYKPGTSYKLSCKGTYFTSYMMHWKQRPQG 63
 DB 1 SCIMFLAATATGVSQVQLQPGAEIYKPGASVYKLSCKASGYFTSYMMHWKQRPGRG 60
 QY 64 LEWIGELIDPESNTNINQKFKKATLTVDISSSTAYWQLSLTSEDSAVYYCAR 123
 DB 61 LEWIGRIDPNSGGTKYNEKFKKATLTVDISSSTAYWQLSLTSEDSAVYYCAR 115
 QY 124 DYALDYGQGTSTVSS 140
 DB 115 DLG-XYWGQGTITLVSS 130

RESULT 14

HYMS3
 Ig heavy chain precursor V region (3) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 23-Aug-1996
 C:Accession: A02031
 R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Karl, T.; Rajewsky, K.; Baltimore, D.
 Cell 24, 625-637, 1981
 A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som
 A:Reference number: A90809; MID:81234548
 A:Accession: A02031
 A:Molecule type: DNA
 A:Residues: 1-117 <BOT>
 A>Note: the sequence was determined from the germline gene
 A>Note: the germline gene, cloned from a library of strain C57BL/6 DNA, is one of a set
 1 (NP antibodies)
 C:Genetics: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (3) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.7%; Score 543; DB 1; Length 117;
 Best Local Similarity 88.0%; Pred. No. 3.2e-40;
 Matches 103; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MGSCLFLVSTATSVHSQVQLQPGAEIYKPGTSYKLSCKGTYFTSYMMHWKQRP 60
 DB 1 MGSCLFLVATATGVSQVQLQPGAEIYKPGSSVYKLSCKASGYFTSYMMHWKQRP 60
 QY 61 GGLLEWIGELIDPESNTNINQKFKKATLTVDISSSTAYWQLSLTSEDSAVYYCAR 117
 DB 61 GGLLEWIGNYPSDSETHYKFKKATLTVDKSSSTAYWQLSLTSEDSAVYYCAR 117

RESULT 15

HYMS61
 Ig heavy chain precursor V region (186-1) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 23-Aug-1996
 C:Accession: D90809; A02036; B02034
 R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Karl, T.; Rajewsky, K.; Baltimore, D.
 Cell 24, 625-637, 1981
 A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som

A:Reference number: A90809; MID:81234548
 A:Accession: D90809
 A:Molecule type: DNA
 A:Residues: 1-117 <BOT>
 A>Note: the sequence was determined from the germline gene
 A>Note: the 186-1 germline gene, cloned from a library of strain C57BL/6 DNA, belongs
 C:Genetics: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (186-1) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 537; DB 1; Length 117;
 Best Local Similarity 84.6%; Pred. No. 1e-39;
 Matches 99; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MGSCLFLVSTATSVHSQVQLQPGAEIYKPGTSYKLSCKGTYFTSYMMHWKQRP 60
 DB 1 MGSCLFLAATATGVSQVQLQPGAEIYKPGASVYKLSCKASGYFTSYMMHWKQRP 60
 QY 61 GGLLEWIGELIDPESNTNINQKFKKATLTVDISSSTAYWQLSLTSEDSAVYYCAR 117
 DB 61 GGLLEWIGRIDPNSGGTKYNEKFKKATLTVDISSSTAYWQLSLTSEDSAVYYCAR 117

Search completed: May 11, 1999, 12:23:24
 Job time: 297 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:20:08 ; Search time 22.45 Seconds
(without alignments)
167.378 Million cell updates/sec

Title: US-08-700-737-15

Perfect score: 757
Sequence: 1 MGSCTILFLVSTFATSVHSQ.....DGMVDAIDYWGCGTSTVSS 140

Scoring table: BLOSUM62

Searched: 74019 seqs, 26840295 residues

Database: SwissProt_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	599.5	79.2	139	1	HV07_MOUSE
2	559	73.8	138	1	HV48_MOUSE
3	556	73.4	117	1	HV06_MOUSE
4	554.5	73.2	137	1	HV11_MOUSE
5	543	71.7	117	1	HV05_MOUSE
6	537	70.9	117	1	HV09_MOUSE
7	532	70.3	140	1	HV02_MOUSE
8	527	69.6	117	1	HV04_MOUSE
9	525	69.4	117	1	HV49_MOUSE
10	519	68.6	117	1	HV10_MOUSE
11	497	65.7	136	1	HV15_MOUSE
12	479.5	63.3	120	1	HV50_MOUSE
13	468	61.8	120	1	HV03_MOUSE
14	447	59.0	121	1	HV01_MOUSE
15	447	59.0	117	1	HV12_MOUSE
16	446	58.9	117	1	HV52_MOUSE
17	445	58.8	117	1	HV13_MOUSE
18	444	58.7	117	1	HV14_MOUSE
19	441.5	58.3	118	1	HV51_MOUSE
20	415.5	54.9	143	1	HV1G_HUMAN
21	412	54.4	117	1	HV1G_HUMAN
22	398	52.6	117	1	HV18_HUMAN
23	348	46.0	117	1	HV42_MOUSE
24	347.5	45.9	114	1	HV00_MOUSE
25	341.5	45.1	136	1	HV16_MOUSE
26	341.5	45.1	119	1	HV38_MOUSE
27	339	44.8	142	1	HV01_RAT
28	335	44.3	117	1	HV41_MOUSE
29	333.5	44.1	119	1	HV37_MOUSE
30	331.5	43.8	146	1	HV21_HUMAN
31	327	43.2	118	1	HV39_MOUSE
32	325.5	43.0	119	1	HV40_MOUSE
33	319	42.1	121	1	HV3J_HUMAN
34	316	41.7	125	1	HV1E_HUMAN
35	312	41.1	117	1	HV1A_HUMAN
36	311.5	41.1	122	1	HV3G_HUMAN
37	308	40.7	115	1	HV32_MOUSE
38	306.5	40.5	126	1	HV3K_HUMAN
39	306	40.4	113	1	HV30_MOUSE
40	305.5	40.4	120	1	HV1H_HUMAN
41	304	40.2	116	1	HV36_MOUSE
42	303.5	40.1	124	1	HV1D_HUMAN
43	302.5	40.0	111	1	HV35_MOUSE

ALIGNMENTS

RESULT 1	ID	HV07_MOUSE	STANDARD:	PRT:	139 AA.	P01794 mus muscula
AC	P01751:	P01752:				P01796 mus muscula
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)					
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)					
DE	IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).					
OS	MUS MUSCULUS (MUSE).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; RODENTIA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-C57BL/6;					
RC	MEDLINE: 81234548.					
RA	BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,					
RL	BALTIMORE D.;					
RL	CELL 24:625-637(1981).					
CC	-1- THE B1-8 MY CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING					
CC	ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB					
CC	ANTIBODIES).					
DR	EMBL: J00529; G195115; -					
DR	PIR: A02034; MEMS18.					
DR	HSSP: P01810; 1JHL.					
KW	IMMUNOGLOBULIN V REGION; SIGNAL.					
FT	SIGNAL	1	19			
FT	CHAIN	20	139			
FT	DOMAIN	20	49			
FT	DOMAIN	50	54			
FT	DOMAIN	55	68			
FT	DOMAIN	69	85			
FT	DOMAIN	86	117			
FT	DOMAIN	118	124			
FT	DOMAIN	125	139			
FT	DOMAIN	41	115			
FT	DISULFID	139	139			
FT	NON_TER	139	139			
SO	SEQUENCE	139 AA;	15419 MW;	DEB2C7DA CRC32;		

Query Match 79.2%; Score 599.5; DB 1; Length 139;
Best Local Similarity 80.7%; Pred. No. 2.4e-50;
Matches 113; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

QY	1	MGSCTILFLVSTFATSVHSQVOLOOPEALYKRGTSYKLSCKGYTFETSYMHWKORP	60
DB	1	MGSCTILFLVSTFATSVHSQVOLOOPEALYKRGTSYKLSCKGYTFETSYMHWKORP	60
QY	61	GQGLEWIGEIDPESNTNNTNQKFKKATLVDISSTAYVQSLNSEDSAVYTCARGY	120
DB	61	GRGLEWIGRIDPNSGGKTKYKFKRSKATLVDPSPSTAYVQSLNSEDSAVYTCARGY	120
QY	121	DGMVDAIDYWGCGTSTVSS	140
DB	121	YGSSY-FDYWGCGTTLVSS	139
RESULT 2			
ID	HV48_MOUSE	STANDARD:	PRT: 138 AA.
AC	P03980;		
DT	23-OCT-1986 (REL. 02, CREATED)		
DT	23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)		
DT	01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)		
DE	IG HEAVY CHAIN PRECURSOR V REGION (TEPC 1017).		
OS	MUS MUSCULUS (MUSE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		

OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84248078.
RA GILLIAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F.,
RA TUCKER P.W.,
RL PROC. NATL. ACAD. SCI. U.S.A. 81:4164-4168(1984).
DR HSP; A02033; HWST7.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION (TRPC 1017).
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; BFF6247B CRC32;

Query Match 73.8%; Score 559; DB 1; Length 138;
Best Local Similarity 75.9%; Pred. No. 1.7e-46;
Matches 107; Conservative 12; Mismatches 18; Indels 4; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHSOVOLQOPGAELVKPGTSVKLSCKGYFTSYMMHWKORP 60
DB 1 MGWSCIILFLVATATGVSHVQLOOPGAELVKPGASVYKSCASGYFTSYMMHWKORP 60
QY 61 GGGLEWIGEIDPSSENNYNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCAR-G 119
DB 61 GGGLEWIGEIDPSSENNYNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCARSDG 120
QY 120 YGDWDYALDWGQSTVTVSS 140
DB 121 YDWD---FVWGQGTTLVTFSA 138

RESULT 3
HVO6_MOUSE STANDARD; PRT; 117 AA.
ID HVO6_MOUSE
AC P01750;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (102).
OS MUS MUSCULUS (MUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6;
RX MEDLINE; 81334548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTIMORE D.;
RL CELL. 24:625-637(1981).
CC -1- THIS GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
DR HSP; A02032; HWMS2.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (102).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12867 MW; 4BDD1982 CRC32;

Query Match 73.4%; Score 556; DB 1; Length 117;
Best Local Similarity 89.7%; Pred. No. 2.7e-46;
Matches 104; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSOVOLQOPGAELVKPGTSVKLSCKGYFTSYMMHWKORP 60
DB 1 MGWSCIILFLVATATGVSHVQLOOPGAELVKPGASVYKSCASGYFTSYMMHWKORP 60
QY 61 GGGLEWIGEIDPSSENNYNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCA 116
DB 61 GGGLEWIGEIDPSSENNYNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCA 116

RESULT 4
HVL1_MOUSE STANDARD; PRT; 137 AA.
ID HVL1_MOUSE
AC P01755;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (S43).
OS MUS MUSCULUS (MUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81334548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTIMORE D.;
RL CELL. 24:625-637(1981).
CC -1- THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NP8
CC ANTIBODIES).
DR EMBL; J00539; G195119; -.
DR PIR; A02038; G2MS43.
DR HSP; P01772; 1FGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION (S43).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; C37539BD CRC32;

Query Match 73.2%; Score 554.5; DB 1; Length 137;
Best Local Similarity 74.1%; Pred. No. 4.5e-46;
Matches 106; Conservative 9; Mismatches 19; Indels 9; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHSOVOLQOPGAELVKPGTSVKLSCKGYFTSYMMHWKORP 60
DB 1 MGWSCIILFLVATATGVSHVQLOOPGAELVKPGASVYKSCASGYFTSYMMHWKORP 60
QY 61 GGGLEWIGEIDPSSENNYNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCAR--- 118
DB 61 GGGLEWIGEIDPSSENNYNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCAR 120
QY 118 GYDWDYALDWGQSTVTVSS 140
DB 121 GRV-----EDYWGQGTTLVSS 137
RESULT 5
HVO5_MOUSE

ID HV05_MOUSE STANDARD; PRT; 117 AA.
 AC P01749;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (3).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE: 81234548.
 RA BOTHEWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 RA BALTIMORE D.;
 RL CELL 24:625-637(1981).
 CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 CC THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
 DR EMBL: J00536; G534035; -.
 DR PIR: A02031; HYMS3.
 DR HSSP: P01810; 1JHL.
 KM IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (3).
 FT DOMAIN 20 49 FRAMEWORK 1.
 AC P01746;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (9367).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 RX MEDLINE: 82152818.
 RA CAPRA J.D., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
 RA SIMS J.,
 RL SCIENCE 215:309-311(1982).
 DR EMBL: J00493; G195007; -.
 DR PIR: A02028; HYMSG7.
 DR HSSP: P01789; 6FAB.
 KM IMMUNOGLOBULIN V REGION; ANTIBODY; HYBRIDOMA; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION (9367).
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA; 15514 MW; 0700D5C8 CRC32;

Query Match 71.7%; Score 543; DB 1; Length 117;
 Best Local Similarity 88.0%; Pred. No. 4.6e-45;
 Matches 103; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 1 MGWSCIIFLVSTATSVHSOVOLQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
 DB 1 MGWSCIIFLVSTATSVHSOVOLQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
 OY 61 GQGLEWIGIDPESNTNTNOKFKRATLTVDISSTAYWQSLTSEDSAVYYCAR 117
 DB 61 GQGLEWIGIDPESNTNTNOKFKRATLTVDISSTAYWQSLTSEDSAVYYCAR 117

RESULT 6
 HV09_MOUSE STANDARD; PRT; 117 AA.

ID HV09_MOUSE STANDARD; PRT; 117 AA.
 AC P01753; P11271;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (186-1).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE: 81234548.
 RA BOTHEWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 RA BALTIMORE D.;
 RL CELL 24:625-637(1981).
 CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 CC THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
 DR PIR: B02034; HYMS61.
 DR HSSP: P01810; 1FVB.
 KM IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (186-1).
 FT DOMAIN 20 49 FRAMEWORK 1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12890 MW; C97683A2 CRC32;

Query Match 70.9%; Score 537; DB 1; Length 117;
 Best Local Similarity 84.6%; Pred. No. 1.7e-44;
 Matches 99; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

OY 1 MGWSCIIFLVSTATSVHSOVOLQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
 DB 1 MGWSCIIFLVSTATSVHSOVOLQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
 OY 61 GQGLEWIGIDPESNTNTNOKFKRATLTVDISSTAYWQSLTSEDSAVYYCAR 117
 DB 61 GQGLEWIGIDPESNTNTNOKFKRATLTVDISSTAYWQSLTSEDSAVYYCAR 117

RESULT 7

HV02_MOUSE STANDARD; PRT; 140 AA.

ID HV02_MOUSE STANDARD; PRT; 140 AA.
 AC P01746;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (9367).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 RX MEDLINE: 82152818.
 RA CAPRA J.D., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
 RA SIMS J.,
 RL SCIENCE 215:309-311(1982).
 DR EMBL: J00493; G195007; -.
 DR PIR: A02028; HYMSG7.
 DR HSSP: P01789; 6FAB.
 KM IMMUNOGLOBULIN V REGION; ANTIBODY; HYBRIDOMA; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION (9367).
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA; 15514 MW; 0700D5C8 CRC32;

Query Match 70.3%; Score 532; DB 1; Length 140;
 Best Local Similarity 72.1%; Pred. No. 6.2e-44;
 Matches 101; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

OY 1 MGWSCIIFLVSTATSVHSOVOLQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
 DB 1 MGWSCIIFLVSTATSVHSOVOLQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
 OY 61 GQGLEWIGIDPESNTNTNOKFKRATLTVDISSTAYWQSLTSEDSAVYYCAR 120
 DB 61 GQGLEWIGIDPESNTNTNOKFKRATLTVDISSTAYWQSLTSEDSAVYYCAR 120
 OY 121 DGMDYADYWGQSTVYSS 140
 DB 121 YGGSYDYWGQSTVYSS 140

RESULT 8

HV04_MOUSE STANDARD; PRT; 117 AA.

ID HV04_MOUSE STANDARD; PRT; 117 AA.
 AC P01748;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (23).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE: 81234548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,
RL CELL 24:625-637(1981).
CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
DR PIR: A02030; HVMS23.
DR HSP: P01810; JHHL.
KM IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (23).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; 66B34D1A CRC32;

Query Match 69.6%; Score 527; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 1.5e-43;
Matches 98; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

OY 1 MGWSCIILFLVSTATSVHSOVOLQOPGAEIVKPGTSYKLSCKGYFTSYMMHWKQRP 60
DB 1 MGWSCIILFLVAAANGHVSQVLOQPGELVKPGASVYKLSCKASGYFTSYMMHWKQRP 60
OY 61 GGGLEWIGELDPSESNNTYNOKFKGKATLVNDISSSTAYVMOSSLTSEDSAVYYCAR 117
DB 61 GGGLEWIGINIPNGNGTNNYNEKFKSKYTLTVDKSSSTAYVMOSSLTSEDSAVYYCAR 117

RESULT 9
HVA9_MOUSE
ID HV49_MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH558 B4).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85099340.
RA YANCOPOULOS G.D., ALT F.W.;
RL CELL 40:271-281(1985).
DR EMBL: M13788; G466292; -.
DR PIR: A02035; MHMSB4.
DR HSP: P01810; JHHL.
KM IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (VH558 B4).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; 85692FE5 CRC32;

Query Match 69.4%; Score 525; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 2.3e-43;
Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

OY 1 MGWSCIILFLVSTATSVHSOVOLQOPGAEIVKPGTSYKLSCKGYFTSYMMHWKQRP 60
DB 1 MGWSCIILFLVAAATGVSFVLOQPGAEIVKPGASVYKLSCKASGYFTSYMMHWKQRP 60
OY 61 GGGLEWIGELDPSESNNTYNOKFKGKATLVNDISSSTAYVMOSSLTSEDSAVYYCAR 117
DB 61 GGGLEWIGINIPNGNGTNNYNEKFKSKYTLTVDKSSSTAYVMOSSLTSEDSAVYYCTR 117

RESULT 10
HVA10_MOUSE
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (145).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE: 81234548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,
RL CELL 24:625-637(1981).
CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
DR EMBL: J00533; G54033; -.
DR PIR: C02034; HVMS45.
DR HSP: P01810; JHHL.
KM IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (145).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D9EBB000 CRC32;

Query Match 68.6%; Score 519; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 8.6e-43;
Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

OY 1 MGWSCIILFLVSTATSVHSOVOLQOPGAEIVKPGTSYKLSCKGYFTSYMMHWKQRP 60
DB 1 MGWSCIILFLVAAATGVSFVLOQPGAEIVKPGASVYKLSCKASGYFTSYMMHWKQRP 60
OY 61 GGGLEWIGELDPSESNNTYNOKFKGKATLVNDISSSTAYVMOSSLTSEDSAVYYCAR 117
DB 61 GGGLEWIGRIDPNNGGTYNEKFKSKYTLTVDKSSSTAYVMOSSLTSEDSAVYYCAR 117

RESULT 11
HVA15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (BC11).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.

[1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE; 82222262.
 RA KNAPP M.R., LIU C.-P., NEWELL N., WARD R.B., TUCKER P.W., STROBER S.,
 BLATTNER F.R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 79:2996-3000(1982).
 DR EMBL; J00494; G195011; -.
 DR HSSP; P01789; 1JEL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL
 FT CHAIN 1
 FT NON_TER 20 136 IG HEAVY CHAIN V REGION (BC11).
 FT SEQUENCE 136 AA; 15078 MW; E04FLC7F CRC32;

Query Match 65.7%; Score 497; DB 1; Length 136;
 Best Local Similarity 68.3%; Pred. No. 1.3e-40;
 Matches 97; Conservative 12; Mismatches 25; Indels 8; Gaps 2;

QY 1 MGMSCTILFVYATATGHSQVLOOQGAELVPGSTVYKLSCKGYGTFTSYMMHWKORP 60
 DB 1 MGMSCTILFVYATATGHSQVLOOQSGREVPRGVSVKISCKSGTITTDAMHWKOSH 60
 QY 61 GQGLEWIGELDPSSNTYNNOKFKGKATLVDISSTAYMQLSLTSDSAVYTCAR--G 118
 DB 61 AKSLEWIGVISTYNGNTSYNNOKFKGKATMTVDKSSVYHMLARLTSDBANLYCARVYG 120
 QY 119 GYDGDVAIDYWGQSTVYSS 140
 DB 121 NY-----FDYWGQGTTLTVSS 136

RESULT 12
 HV03_MOUSE STANDARD; PRT; 120 AA.
 AC P06329;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DE 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (AC38 15.3).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RA MEDLINE; 84182519.
 RA DILDROP R., BOVENS J., SIEKEVITZ M., BEYREUTHER K., RAJEMSKY K.;
 RL EMBL J. 3:517-523(1984).
 DR PIR; A02037; MMS15.
 DR HSSP; P01772; 1FGV.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 98
 FT DOMAIN 99 105 V SEGMENT.
 FT DOMAIN 106 120 D SEGMENT.
 FT DISULFID 22 96 J SEGMENT.
 FT NON_TER 120 120 BY SIMILARITY.
 FT SEQUENCE 120 AA; 13311 MW; 85EC01BA CRC32;

Query Match 63.3%; Score 479.5; DB 1; Length 120;
 Best Local Similarity 75.2%; Pred. No. 5e-39;
 Matches 91; Conservative 7; Mismatches 22; Indels 1; Gaps 1;

QY 20 QVLOQPAELVPGSTVYKLSCKGYGTFTSYMMHWKORPQGLEWIGELDPSSNTY 79
 DB 1 QVLOQPAELVPGSTVYKLSCKASGYFTSYMMHWKORPQGLEWIGISNGNTY 60
 QY 80 NOKFKGKATLVDISSTAYMQLSLTSDSAVYTCARQGMVAIDYWGQSTVYSS 139
 DB 61 NEKFKGKATLVDISSTAYMQLSLTSDSAVYTCARQGMV--DRYDVGQGTTLTVSS 119
 QY 140 S 140

DB 120 S 120

RESULT 13
 HV03_MOUSE STANDARD; PRT; 120 AA.
 AC P01747;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (36-65).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 83131846.
 RA SIEKEVITZ M., GELTER M.L., BRODEUR P., RIBLET R.,
 MARSHAK-ROTHSTEIN A.;
 RL EUR. J. IMMUNOL. 12:1023-1032(1982).
 CC -1- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
 THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF
 THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.
 DR PIR; A02028; HVMSC7.
 DR HSSP; P01789; 6PAB.
 KW IMMUNOGLOBULIN V REGION; ANTIBODYSOMATE ANTIBODY; HYBRIDOMA.
 FT NON_TER 120 120
 FT SEQUENCE 120 AA; 13307 MW; BBAGCA1 CRC32;

Query Match 61.8%; Score 468; DB 1; Length 120;
 Best Local Similarity 74.2%; Pred. No. 6.1e-38;
 Matches 89; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 21 VQLOQPAELVPGSTVYKLSCKGYGTFTSYMMHWKORPQGLEWIGELDPSSNTY 80
 DB 1 VQLOQPAELVPGSTVYKLSCKASGYGTFTSYMMHWKORPQGLEWIGYINPGNYTXN 60
 QY 81 OKFKGKATLVDISSTAYMQLSLTSDSAVYTCARQGMVAIDYWGQSTVYSS 140
 DB 61 EKFKGKATLVDISSTAYMQLSLTSDSAVYTCARQGMVYGGSYFDYWGQGTTLTVSS 120

RESULT 14
 HV01_MOUSE STANDARD; PRT; 121 AA.
 AC P01745;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 13-AUG-1987 (REL. 05, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (MPC 11).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 81053741.
 RA ZAKUT R., COHEN J., GIOVOL D.;
 RL NUCLEIC ACIDS RES. 8:3591-3601(1980).
 RL [2]
 RP REVISIONS.
 RA ZAKUT R., COHEN J., GIOVOL D.;
 RL NUCLEIC ACIDS RES. 8:4839-4840(1980).
 CC -1- THIS SEQUENCE WAS TRANSLATED FROM AN mRNA ISOLATED FROM A
 MYELOMA THAT SECRETES IGG2B.
 DR PIR; A02027; GVM511.
 DR HSSP; P01810; 1MFE.
 KW IMMUNOGLOBULIN V REGION.
 FT NON_TER 121 121
 FT SEQUENCE 121 AA; 13135 MW; 2A8FC8CC CRC32;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:21:01 ; Search time 38.54 seconds
(without alignments)
200.407 Million cell updates/sec

Title: US-08-700-737-15

Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHSQ.....DGM DYALDYWGGSITVSS 140

Scoring table: BLOSUM62

Searched: 180763 seqs, 55169189 residues

Database : SPTREMBL_8:*
1: sp_fungi:*
2: sp_human:*
3: sp_invertebrate:*
4: sp_mammal:*
5: sp_mmc:*
6: sp_organelle:*
7: sp_phage:*
8: sp_plant:*
9: sp_bacteria:*
10: sp_rodent:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_unclassified:*
14: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	213.5	28.2	85	2	075724	075724 homo sapien
2	212	28.0	82	2	075729	075729 homo sapien
3	203	26.8	88	2	075737	075737 homo sapien
4	202	26.7	76	2	075742	075742 homo sapien
5	196	25.9	77	2	075741	075741 homo sapien
6	188.5	24.9	81	2	075719	075719 homo sapien
7	188.5	24.9	77	2	075726	075726 homo sapien
8	187.5	24.8	78	2	075730	075730 homo sapien
9	187	24.7	77	2	075728	075728 homo sapien
10	185.5	24.5	81	2	075734	075734 homo sapien
11	182.5	24.1	82	2	075725	075725 homo sapien
12	181	23.9	86	2	075740	075740 homo sapien
13	181	23.9	74	2	075744	075744 homo sapien
14	179	23.6	78	2	075723	075723 homo sapien
15	178	23.5	86	2	075722	075722 homo sapien
16	176	23.2	72	2	075738	075738 homo sapien
17	175.5	23.2	81	2	075721	075721 homo sapien
18	174.5	23.1	80	2	075727	075727 homo sapien
19	173	22.9	80	2	075735	075735 homo sapien
20	171.5	22.7	79	2	075731	075731 homo sapien
21	169	22.3	76	2	075733	075733 homo sapien
22	167	22.1	82	2	075732	075732 homo sapien
23	165.5	21.9	81	2	075736	075736 homo sapien
24	163	21.5	78	2	075739	075739 homo sapien
25	159.5	21.1	75	2	075743	075743 homo sapien
26	157.5	20.8	97	2	043234	043234 homo sapien
27	151	19.9	45	2	076051	076051 homo sapien
28	149	19.7	78	2	075720	075720 homo sapien
29	147	19.4	145	2	016237	016237 homo sapien

30	122	16.1	64	10	061750	061750 mus musculu
31	119	15.7	130	10	P80913	P80913 mus musculu
32	116	15.3	135	5	Q31174	Q31174 mus musculu
33	115.5	15.3	119	2	099601	099601 homo sapien
34	114	15.1	119	2	099599	099599 homo sapien
35	109.5	14.5	121	2	099600	099600 homo sapien
36	104.5	13.8	254	12	Q90557	Q90557 ginglymosto
37	100.5	13.3	123	10	061243	061243 mus musculu
38	99	13.1	122	2	099603	099603 homo sapien
39	98.5	13.0	134	5	Q31180	Q31180 mus musculu
40	97.5	12.9	213	5	Q31127	Q31127 mus musculu
41	97	12.8	157	12	Q90539	Q90539 ginglymosto
42	95.5	12.6	137	5	Q31181	Q31181 mus musculu
43	95	12.5	210	4	P79336	P79336 felis silve
44	93.5	12.4	258	12	Q90559	Q90559 ginglymosto
45	93	12.3	122	2	Q99604	Q99604 homo sapien

ALIGNMENTS

RESULT	ID	Score	Match	Length	DB	ID	Description
1	075724	213.5	28.2	85	2	075724	075724 homo sapien
2	075729	212	28.0	82	2	075729	075729 homo sapien
3	075737	203	26.8	88	2	075737	075737 homo sapien
4	075742	202	26.7	76	2	075742	075742 homo sapien
5	075741	196	25.9	77	2	075741	075741 homo sapien
6	075719	188.5	24.9	81	2	075719	075719 homo sapien
7	075726	188.5	24.9	77	2	075726	075726 homo sapien
8	075730	187.5	24.8	78	2	075730	075730 homo sapien
9	075728	187	24.7	77	2	075728	075728 homo sapien
10	075734	185.5	24.5	81	2	075734	075734 homo sapien
11	075725	182.5	24.1	82	2	075725	075725 homo sapien
12	075740	181	23.9	86	2	075740	075740 homo sapien
13	075744	181	23.9	74	2	075744	075744 homo sapien
14	075723	179	23.6	78	2	075723	075723 homo sapien
15	075722	178	23.5	86	2	075722	075722 homo sapien
16	075738	176	23.2	72	2	075738	075738 homo sapien
17	075721	175.5	23.2	81	2	075721	075721 homo sapien
18	075727	174.5	23.1	80	2	075727	075727 homo sapien
19	075735	173	22.9	80	2	075735	075735 homo sapien
20	075731	171.5	22.7	79	2	075731	075731 homo sapien
21	075733	169	22.3	76	2	075733	075733 homo sapien
22	075732	167	22.1	82	2	075732	075732 homo sapien
23	075736	165.5	21.9	81	2	075736	075736 homo sapien
24	075739	163	21.5	78	2	075739	075739 homo sapien
25	075743	159.5	21.1	75	2	075743	075743 homo sapien
26	043234	157.5	20.8	97	2	043234	043234 homo sapien
27	076051	151	19.9	45	2	076051	076051 homo sapien
28	075720	149	19.7	78	2	075720	075720 homo sapien
29	016237	147	19.4	145	2	016237	016237 homo sapien

ID 075734 PRELIMINARY; PRT; 81 AA.
AC 075734;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE-INTESINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
RT mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AJ009531; E1311462; -.
FT NON_TER 1 81
FT NON_TER 1 81
SQ SEQUENCE 81 AA; 9040 MW; 56B4D902 CRC32;

Query Match 24.5%; Score 185.5; DB 2; Length 81;
Best Local Similarity 42.0%; Pred. No. 2.9e-11;
Matches 34; Conservative 16; Mismatches 24; Indels 7; Gaps 1;

QY 50 SYMMHWKORPGGLEWIGELIDPSESNTYNOFKFKATLTVDISSTAYMQLSLTSED 109
DB 1 SYMMHWKORPGGLEWIGELIDPSESNTYNOFKFKATLTVDISSTAYMQLSLTSED 60
QY 110 SAVYYCAR-----GGYDGM 123
DB 61 TAVYYCARVLTNYKYPNGMDVM 81

RESULT 11
ID 075725 PRELIMINARY; PRT; 82 AA.
AC 075725;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE-INTESINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
RT mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AJ009522; E1311444; -.
FT NON_TER 1 82
FT NON_TER 1 82
SQ SEQUENCE 82 AA; 9566 MW; 1F2E1379 CRC32;

Query Match 24.1%; Score 182.5; DB 2; Length 82;
Best Local Similarity 45.1%; Pred. No. 5.7e-11;
Matches 37; Conservative 16; Mismatches 24; Indels 5; Gaps 4;

QY 51 YMMHWKORPGGLEWIGELIDPSESNTYNOFKFKATLTVDISSTAYMQLSLTSED 110
DB 4 YMMHWKORPGGLEWIGELIDPSESNTYNOFKFKATLTVDISSTAYMQLSLTSED 61
QY 111 AVYYCAR--GGYDGMVAIDYM 130
DB 62 AVYYCARPFGGRAWPY-FDIW 82

RESULT 12
ID 075740 PRELIMINARY; PRT; 86 AA.
AC 075740;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE-INTESINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
RT mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AJ009539; E1311474; -.
FT NON_TER 1 86
FT NON_TER 1 86
SQ SEQUENCE 86 AA; 9625 MW; 07627E8C CRC32;

Query Match 23.9%; Score 181; DB 2; Length 86;
Best Local Similarity 48.5%; Pred. No. 8.3e-11;
Matches 32; Conservative 14; Mismatches 18; Indels 2; Gaps 1;

QY 52 WMHWKORPGGLEWIGELIDPSE--SNTYNOFKFKATLTVDISSTAYMQLSLTSED 109
DB 3 WMHWKORPGGLEWIGELIDPSE--SNTYNOFKFKATLTVDISSTAYMQLSLTSED 62
QY 110 SAVYYC 115
DB 63 TAVYYC 68

RESULT 13
ID 075744 PRELIMINARY; PRT; 74 AA.
AC 075744;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE-INTESINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
RT mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AJ009545; E1311484; -.
FT NON_TER 1 74
FT NON_TER 1 74
SQ SEQUENCE 74 AA; 8541 MW; 46693A8A CRC32;

Query Match 23.9%; Score 181; DB 2; Length 74;
Best Local Similarity 40.5%; Pred. No. 7.1e-11;
Matches 32; Conservative 14; Mismatches 27; Indels 6; Gaps 1;

QY 52 WMHWKORPGGLEWIGELIDPSESNTYNOFKFKATLTVDISSTAYMQLSLTSED 111
DB 2 WMHWKORPGGLEWIGELIDPSESNTYNOFKFKATLTVDISSTAYMQLSLTSED 61
QY 112 VYICARGYDGMVAIDYM 130

Db 62 VYCAATG-----PALDLW 74

RESULT 14

ID 075723 PRELIMINARY; PRT: 78 AA.

AC 075723; 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RP SEQUENCE FROM N.A.

RA FISCHER M., KUEPPERS R.; Human IgA and IgM secreting intestinal plasma cells carry heavily

RT mutated VH region genes.

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

FT NON_TER 1 1

FT NON_TER 78 78

SEQ SEQUENCE 78 AA; 9075 MW; DFEED569 CRC32;

Query Match 23.6%; Score 179; DB 2; Length 78;

Best Local Similarity 49.2%; Pred. No. 1.2e-10; Matches 31; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 55 WKQPGGGLWGEIDPESNTNYNOKFKATLVDISSTAYMQLSTSEDSAVYY 114

Db 1 WVRQAPGKGLWVYARISSESRINYADSVKGFISRDNAKNTLYLQNSLRADTAVYY 60

QY 115 CAR 117

Db 61 CAR 63

RESULT 15

ID 075722 PRELIMINARY; PRT: 86 AA.

AC 075722; 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RP SEQUENCE FROM N.A.

RA FISCHER M., KUEPPERS R.; Human IgA and IgM secreting intestinal plasma cells carry heavily

RT mutated VH region genes.

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

FT NON_TER 1 1

FT NON_TER 86 86

SEQ SEQUENCE 86 AA; 9769 MW; 5F6AC773 CRC32;

Query Match 23.5%; Score 178; DB 2; Length 86;

Best Local Similarity 41.2%; Pred. No. 1.6e-10; Matches 35; Conservative 17; Mismatches 29; Indels 4; Gaps 2;

QY 50 SYMHVWQKRGGLWGEIDPESNTNYNOKFKATLVDISSTAYMQLSTSEDS 109

Db 2 SHMKVWQKRGGLWGEIDPESNTNYNOKFKATLVDISSTAYMQLSTSEDS 61

QY 110 SAVYYCA--RGYDGMW--YAIQW 130

Db 62 TAVYYCARQGAAGCTDYQGMW 86

Search completed: May 11, 1999, 12:21:01
Job time: 253 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:14:53 ; Search time 44.09 seconds
(without alignments)
64.222 Million cell updates/sec

Title: US-08-700-737-15

Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHSQ.....DGMVDYALDYGQGTSTVYSS 140

Scoring table: BLOSUM62

Searched: 162890 seqs, 20225328 residues

Database: A_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	757	100.0	140	1	Murine Act-1 heavy
2	730	96.4	137	1	Protein sequence o
3	713	94.2	144	1	Consensus protein
4	632	83.5	180	1	Heavy chain of a h
5	597	78.9	464	1	MAB 55.1 heavy cha
6	594.5	78.5	443	1	Single chain anti
7	589	77.8	140	1	VH425 antibody c10
8	586	77.4	136	1	Sequence encoded b
9	586	77.4	136	1	Chimeric anti-hepa
10	586	77.4	136	1	Mouse-human chime
11	586	77.4	136	1	Anti-hepatitis B h
12	586	77.4	136	1	Human anti-hepatit
13	586	77.4	136	1	Human anti-hepatit
14	586	77.4	136	1	Human anti-hepatit
15	583	77.0	143	1	MAB SCH94.03 heavy
16	551.5	72.9	144	1	Heavy chain variab
17	551.5	72.9	143	1	Mouse MAB 2E12 H C
18	549	72.5	138	1	Amino acid sequenc
19	548.5	72.5	137	1	Monoclonal antibod
20	545	72.0	140	1	Murine variable re
21	544.5	71.9	139	1	p64-h2 protein pro
22	543	71.7	140	1	MAB Co-1 heavy cha
23	538	71.1	119	1	Anti-DNA antibody
24	537	70.9	140	1	Co-1 Heavy Chain V
25	536.5	70.9	145	1	Anti-tobacco mosai
26	536	70.8	119	1	Anti-EGFR antibody
27	532	70.3	138	1	Murine ICR-1.1 V-H
28	532	70.3	138	1	Murine antibody IC
29	531	70.1	136	1	Sequence of the he
30	529.5	69.9	139	1	Heavy chain of mon
31	528.5	69.8	139	1	Anti-HMG MAB CTMO
32	525.5	69.4	428	1	Single chain anti
33	521.5	68.9	139	1	CTMO1 VH. Anti-hum
34	521.5	68.9	269	1	PRAS11 between HI
35	521.5	68.9	435	1	scfv PRAS108 and p
36	521.5	68.9	402	1	scfv PRAS110 and p
37	521.5	68.9	269	1	B-cell lymphoma CH
38	520.5	68.8	122	1	MAB 55.1 heavy cha
39	520	68.7	119	1	Anti-EGFR antibody
40	520	68.7	119	1	Murine antibody he
41	518.5	68.5	118	1	ME4 Heavy Chain V
42	516.5	68.2	141	1	Murine anti-CD18 A
43	516.5	68.2	120	1	

ALIGNMENTS

44 516.5 68.2 141 1 W05216 MAB ME4 heavy chain
45 516.5 68.2 464 1 W14941 3F4 Human IgG4 exp

RESULT 1
ID W53815
AC W53815
DE 14-JUL-1998 (first entry)
KW Murine Act-1 heavy chain variable region.
KW Mouse: Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal adressin cell adhesion molecule-1; MacCAM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW inflammatory bowel disease.
OS Mus sp.
FH Key
FT Peptide 1..19 Location/Qualifiers
FT Protein /note="signal peptide"
FT Protein /note="mature protein"
PN W09806248-A2.
PD 19-FEB-1998.
PF 06-AUG-1997; U13884.
PR 15-AUG-1996; US-700737.
PA (LEUK-) LEUKOSTITE INC.
PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
PI Saldanha J;
DR WPI: 98-159172/14.
DR N-PSDB: V20078.
PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
PT used for treating inflammatory disease, pancreatitis, diabetes,
PT asthma, graft versus host disease and sarcoidosis
PS Claim 27; Fig 9; 145pp; English.
CC The present sequence represents the heavy chain variable region of
CC murine antibody Act-1. Act-1 is active against human alpha4-beta7
CC integrin. Muscosal adressin cell adhesion molecule-1 (MacCAM-1) is a
CC ligand of this particular integrin. The Act-1 antibody interferes with
CC endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used
CC to inhibit the interaction of cells bearing alpha4-beta7 with cells
CC bearing a ligand for alpha4-beta7. It can be used for inhibiting
CC leukocyte infiltration of tissues, e.g. for treating inflammatory
CC diseases such as inflammatory bowel disease. The immunoglobulin can
CC also be used for detection, isolation and diagnosis.
SQ Sequence 140 AA;

Query Match 100.0%; Score 757; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.9e-54;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEVYKPGTSYKLSCKGYGTFTYMHVWKORP 60
DB 1 MGWSCIILFLVSTATSVHSQVLOQPGAEVYKPGTSYKLSCKGYGTFTYMHVWKORP 60
QY 61 GGGLEWIGEIDPESNTNYNQKFKRATLTVDISSSTAYWQSLTSEDSAVYYCARGGY 120
DB 61 GGGLEWIGEIDPESNTNYNQKFKRATLTVDISSSTAYWQSLTSEDSAVYYCARGGY 120
QY 121 DGMVDYALDYGQGTSTVYSS 140
DB 121 DGMVDYALDYGQGTSTVYSS 140
RESULT 2
ID W53818
AC W53818;
DE 14-JUL-1998 (first entry)

DE Protein sequence of murine variable heavy chain region of clone H2B#34.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosa1 addressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease.
 OS Mus sp.
 PN W09806248-A2.
 PD 19-FEB-1998.
 PE 06-AUG-1997: U13884.
 PR 15-AUG-1996: US-700737.
 PA (LEUK-) LEUKOSTITE INC.
 PI Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI: 98-159172/14.
 DR N-PSDB: V20089.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 2; 145pp; English.
 CC The present sequence represents the amino acid sequence comprising the
 CC variable region of murine Act-1 antibody determined from clone H2B#34.
 CC Act-1 is active against human alpha4-beta7 integrin. Muscosa1 addressin
 CC cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular
 CC integrin. The Act-1 antibody interferes with alpha4-beta7 integrin binding
 CC to MadCAM-1, which is present of high endothelial venules in muscosa1
 CC lymph nodes. The present sequence was used to construct chimeric,
 CC humanised Act-1 antibodies, which contain murine antigen binding regions.
 CC The humanised immunoglobulin can be used to inhibit the interaction of
 CC cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7.
 CC It can be used for inhibiting leukocyte infiltration of tissues, e.g. for
 CC treating inflammatory diseases such as inflammatory bowel disease. The
 CC immunoglobulin can also be used for detection, isolation and diagnosis.
 SQ Sequence 137 AA;

Query Match 96.4%; Score 730; DB 1; Length 137;
 Best Local Similarity 98.5%; Pred. No. 9.6e-52;
 Matches 135; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWCIILFLVSTATSVHSOVOLQPGAEIVKPGSVKLSCKGTYTPTSMHWKORP 60
 DB 1 MGWYIILFLVSTATSVHSOVOLQPGAEIVKPGSVKLSCKGTYTPTSMHWKORP 60
 QY 61 GGGLEWIGIDPESSENNYNNQKFKGKATLVDISSTAYMQLSSLTSEDSAVYYCARGGY 120
 DB 61 GGGLEWIGIDPESSENNYNNQKFKGKATLVDISSTAYMQLSSLTSEDSAVYYCARGGY 120
 QY 121 DGMVDAIDYWGQGTSTV 137
 DB 121 DGMVDAIDYWGQGTSTV 137

RESULT 3
 W53816
 ID W53816 standard; Protein; 144 AA.
 AC W53816;
 DT 14-JUL-1998 (first entry)
 DE Consensus protein sequence of the murine variable heavy chain region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosa1 addressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease.
 OS Mus sp.
 PH Key location/Qualifiers
 FT MISC_difference 2 /note- "not specified, encoded by RRA"
 FT MISC_difference 3 /note- "not specified, encoded by TGS"
 FT MISC_difference 4 /note- "not specified, encoded by ASC"
 FT MISC_difference 5

FT /note- "not specified, encoded by TRK"
 FT MISC_difference 6 /note- "not specified, encoded by RNC"
 FT MISC_difference 7 /note- "encoded by ATY"
 FT MISC_difference 8 /note- "not specified, encoded by YNC"
 FT Peptide 1.19 /note- "signal peptide"
 FT Protein 20.144 /note- "mature protein"
 FT Region 20.49 /note- "framework region 1"
 FT Region 50.54 /note- "CDR1"
 FT Region 55.68 /note- "framework region 2"
 FT Region 69.85 /note- "CDR2"
 FT Region 86.117 /note- "framework region 3"
 FT Region 118.130 /note- "CDR3"
 FT Region 131.141 /note- "framework region 4"
 PN W09806248-A2.
 PD 19-FEB-1998.
 PE 06-AUG-1997: U13884.
 PR 15-AUG-1996: US-700737.
 PA (LEUK-) LEUKOSTITE INC.
 PI Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI: 98-159172/14.
 DR N-PSDB: V20085.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 1; 145pp; English.
 CC The present sequence represents the consensus amino acid sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse heavy chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosa1 addressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in muscosa1
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20079-82. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 144 AA;

Query Match 94.2%; Score 713; DB 1; Length 144;
 Best Local Similarity 99.3%; Pred. No. 2.3e-50;
 Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ILFLVSTATSVHSOVOLQPGAEIVKPGSVKLSCKGTYTPTSMHWKORP 66
 DB 7 ILFLVSTATSVHSOVOLQPGAEIVKPGSVKLSCKGTYTPTSMHWKORP 66
 QY 67 IGEIDPESSENNYNNQKFKGKATLVDISSTAYMQLSSLTSEDSAVYYCARGGY 126
 DB 67 IGEIDPESSENNYNNQKFKGKATLVDISSTAYMQLSSLTSEDSAVYYCARGGY 126
 QY 127 IDWVGQSTVTVSS 140
 DB 127 IDWVGQSTVTVSS 140

DB 127 IDYWGQSTVTYSS 140

RESULT 4
W53813
ID W53813 standard; Protein: 180 AA.

AC W53813; 14-JUL-1998 (first entry)
DE Heavy chain of a humanised murine Act-1 antibody.
KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leucocyte infiltration of tissue; treatment; inflammatory disease;
KW inflammatory bowel disease.
OS Synthetic.
OS Mus sp.

OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note="signal peptide"
FT 20..180
FT Protein /note="mature protein"

PN W09806248-A2.
PD 19-FEB-1998.
PF 06-AUG-1997; U13884.
PR 15-AUG-1996; US-700737.
PA (LEUK-) LEUKOSITE INC.

PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ, Saldanha J.
DR WPI: 98-159172/14.
DR N-PSDB: V20076.
PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
PT used for treating inflammatory disease, pancreatitis, diabetes,
PT asthma, graft versus host disease and sarcoidosis
PS Claim 20; Fig 11; 145pp; English.

CC The present sequence represents the heavy chain of humanised murine
CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
CC Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of
CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
CC integrin binding to MadCAM-1, which is present of high endothelial
CC venules in mucosal lymph nodes. The humanised immunoglobulin can be
CC used to inhibit the interaction of cells bearing alpha4-beta7 with
CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
CC leucocyte infiltration of tissues, e.g. for treating inflammatory
CC diseases such as inflammatory bowel disease. The immunoglobulin can
CC also be used for detection, isolation and diagnosis.
SQ Sequence 180 AA;

Query Match 83.5%; Score 632; DB 1; Length 180;

Best Local Similarity 85.9%; Pred. No. 8e-44;
Matches 116; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 6 IILFLVSTATSVHSQVLOQPGAEIVKPGTGVKLSCKGSGYFTSYMMHWKORPGGGL 65
DB 6 VILFLVSTATSVHSQVLOQPGAEIVKPGTGVKLSCKGSGYFTSYMMHWKORPGGRL 65
QY 66 WIEIDPSESNTNNOFKRKATLTVDISSSTAYMQSLSESAVYYCARGGYDWDY 125
DB 66 WIEIDPSESNTNNOFKRKATLTVDISSSTAYMQSLSESAVYYCARGGYDWDY 125
QY 126 AIDYWGQSTVTYSS 140
DB 126 AIDYWGQSTVTYSS 140

RESULT 5
R76088
ID R76088 standard; Protein: 464 AA.
AC R76088;
DT 21-NOV-1995 (first entry)
DE MAb 55.1 heavy chain.
KW Antigen binding structure; complementarity determining region; CDR;

KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin.
OS Mus sp.

FH Key Location/Qualifiers
FT Peptide 1..19
FT /label="sig_peptide"
FT 20..464
FT Protein /label="Mat protein"
FT /note="claim 3, page 97-98"

PN W09515382-A.
PD 08-JUN-1995.
PF 29-NOV-1994; G02610.
PR 03-DEC-1993; GB-024819.
PR 03-JUN-1994; GB-011089.
PA (ZENE) ZENECA LTD.

PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
PI Rose MS, Wright AF;
DR WPI: 95-215262/28.
DR N-PSDB: Q94037.

PT Antigen binding structures containing CDRs recognising the CA55.1
PT antigen - produced by hybridomas and host cells, for use in the
PT diagnosis and therapy of cancer
PS disclosure; Fig.15; 121pp; English.
CC MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
CC antigen CA55.1. cDNAs for the heavy (Q94037) and light (Q94036)
CC chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scfv or
CC v-mim humanized 55.1 constructs have been expressed in myeloma
CC cells and E. coli.
SQ Sequence 464 AA;

Query Match 78.9%; Score 597; DB 1; Length 464;
Best Local Similarity 80.0%; Pred. No. 1.3e-40;
Matches 112; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGNSCIILFLVSTATSVHSQVLOQPGAEIVKPGTGVKLSCKGSGYFTSYMMHWKORP 60
DB 1 MGNSCIILFLVSTATSVHSQVLOQPGAEIVKPGTGVKLSCKGSGYFTSYMMHWKORP 60
QY 61 GGGLEWIGEIDPSESNTNNOFKRKATLTVDISSSTAYMQSLSESAVYYCARGGY 120
DB 61 GGGLEWIGEIDPSESNTNNOFKRKATLTVDISSSTAYMQSLSESAVYYCARERA 120
QY 121 DGYDVAIDYWGQSTVTYSS 140
DB 121 YGYDVAIDYWGQSTVTYSS 140

RESULT 6
W24025
ID W24025 standard; Protein: 443 AA.
AC W24025;
DT 04-MAR-1998 (first entry)
DE Single chain antigen hybrid receptor.
KW Hybrid receptor; single chain antigen; gene therapy; diagnosis;
KW signal conduction; receptor; control region.
OS Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label="leader_peptide"
FT 20..444
FT Protein /note="single chain antigen hybrid receptor"
FT /label="VL_B_1-8"
FT 20..139
FT Region /note="variable heavy chain region of BI-8 antibody"
FT 140..154
FT /label="(Gly_Ser)3"
FT /note="linker region"
FT 155..264
FT /label="VL_B_1-8"

DB 121 D-W---FAYWGGTWTAVSS 136

RESULT 13

W41054
ID W41054 standard; Protein: 136 AA.
AC W41054;
DE Human anti-hepatitis antibody heavy chain.
KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
KW immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody L6; human lung carcinoma cell.
OS Homo sapiens.
PN US5693493-A.
PD 02-DEC-1997.
PF 25-MAY-1995; 450731.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PR 25-MAY-1995; US-450731.
PA (XOMA) XOMA CORP.
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL;
DR WPI: 98-031749/03.
DR N-PSDB: V03836, V03866.
PT Production of chimeric antibody fragments - by culturing E. coli
PT transformed with dicistronic expression cassette
PS Example II: Fig 12B; 98pp; English.
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody L6 raised
CC against human lung carcinoma cells. The invention provides a novel
CC approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
SQ Sequence 136 AA;

Query Match 77.4%; Score 586; DB 1; Length 136;
Best Local Similarity 81.4%; Pred. No. 2.8e-40;
Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHSVOVLOQPGALVYKGTSTYKLSCKGYGTFSTYMMHWKORP 60
DB 1 MGWSCIILFLVATARVHSVOVLOQPGALVYKGTSTYKLSCKGYGTFSTYMMHWKORP 60
QY 61 GGLLEWIGELIDPESNTNNOKFKKATLTVDSSSTAYMOLSLTSEDSAYYYCARGGY 120
DB 61 GGLDWIGELINPNSNGRTNNEKFKSKATLTVDSSSTAYMOLSLTSEDSAYYYCASDY 120
QY 121 DGMWDYALDWGQGTSTVSS 140

DB 121 D-W---FAYWGGTWTAVSS 136

RESULT 14

W47517
ID W47517 standard; Protein: 136 AA.
AC W47517;
DE Human anti-hepatitis antibody heavy chain.
KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
KW immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody L6; human lung carcinoma cell.
OS Homo sapiens.
PN US5698417-A.
PD 16-DEC-1997.
PF 06-JUN-1995; 466203.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PR 25-MAY-1995; US-450731.
PR 06-JUN-1995; US-466203.
PA (XOMA) XOMA CORP.
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL;
DR WPI: 98-051487/05.
DR N-PSDB: V18589, V18590.
PT Production of recombinant immunoglobulin fragment - comprising Fd
PT molecule and light chain
PS Example II: Fig 12B; 98pp; English.
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody L6 raised
CC against human lung carcinoma cells. The invention provides a novel
CC approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
SQ Sequence 136 AA;

Query Match 77.4%; Score 586; DB 1; Length 136;
Best Local Similarity 81.4%; Pred. No. 2.8e-40;
Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHSVOVLOQPGALVYKGTSTYKLSCKGYGTFSTYMMHWKORP 60
DB 1 MGWSCIILFLVATARVHSVOVLOQPGALVYKGTSTYKLSCKGYGTFSTYMMHWKORP 60
QY 61 GGLLEWIGELIDPESNTNNOKFKKATLTVDSSSTAYMOLSLTSEDSAYYYCARGGY 120
DB 61 GGLDWIGELINPNSNGRTNNEKFKSKATLTVDSSSTAYMOLSLTSEDSAYYYCASDY 120

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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 12:00:29 ; Search time 962.98 Seconds

(without alignments)
2006.143 Million cell updates/sec

Title: US-08-700-737-18

Perfect score: 540
Sequence: 1 ATGAATGACACCTGGTGCAT.....CCGAACCGGTGACGGTGTCTCG 540

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database :

GenEmbl.*
1: gb_dal.*
2: gb_ba2.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl1.*
9: gb_pl2.*
10: gb_pr1.*
11: gb_pr2.*
12: gb_pr3.*
13: gb_ro.*
14: gb_st.*
15: gb_sy.*
16: gb_un.*
17: gb_vl.*
18: gb_htg.*
19: em_ba.*
20: em_fun.*
21: em_hum1.*
22: em_hum2.*
23: em_in.*
24: em_om.*
25: em_or.*
26: em_ov.*
27: em_pat.*
28: em_ph.*
29: em_pl.*
30: em_ro.*
31: em_sy.*
32: em_un.*
33: em_vl.*
34: em_htg.*
35: em_st.*
36: gb_ba1.*
37: gb_ba2.*
38: gb_pl1.*
39: gb_pl2.*
40: gb_pl1.*
41: gb_pr2.*
42: gb_pr3.*
43: gb_sts.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length DB	ID	Description

1	354.4	65.6	9209	6	AR000007	AR000007 Sequence
2	354.4	65.6	9209	6	AR015961	AR015961 Sequence
3	329.4	61.0	1572	6	A44967	A44967 Sequence 23
4	329.4	61.0	1572	6	A44967	A44967 Sequence 23
5	327.8	60.7	762	6	I69485	I69485 Sequence 57
6	327.8	60.7	762	6	I73104	I73104 Sequence 57
7	327.8	60.7	762	6	I79289	I79289 Sequence 57
8	327.8	60.7	762	6	I87063	I87063 Sequence 57
9	326.2	60.4	531	10	HDWIGHDJA	L23555 Human IGH C
10	324.8	60.1	1544	13	MUSIGBIHL	L23555 Human IGH C
11	321.6	59.6	1599	10	HDWIGHDJA	D14625 Mouse mRNA
12	321.6	59.6	1599	10	HDWIGHDJA	M87789 Human (hybr
13	318.4	59.0	3282	6	I58595	I58595 Sequence 15
14	318.4	59.0	13254	6	I58596	I58596 Sequence 15
15	318.4	59.0	3282	6	I58609	I58609 Sequence 16
16	318.4	59.0	13254	6	I58610	I58610 Sequence 17
17	317.2	58.7	530	10	HSU43758	U43758 Human Immun
18	317.2	58.7	530	10	HSU43758	U43758 Human Immun
19	317.2	58.7	533	10	HSU43762	U43762 Human Immun
20	317	58.7	533	10	HSU43762	U43762 Human Immun
21	317	58.7	533	10	HSU43762	U43762 Human Immun
22	308.8	57.2	516	10	HS20166	Z47252 H.sapiens m
23	308.8	57.2	516	10	HS20166	Z47252 H.sapiens m
24	306	56.7	522	10	HS20268	Z47260 H.sapiens m
25	306	56.7	522	10	HS20268	Z47260 H.sapiens m
26	305.6	56.6	516	10	HS20162	Z47253 H.sapiens m
27	305.6	56.6	516	10	HS20162	Z47253 H.sapiens m
28	305.6	56.6	516	10	HS20162	Z47253 H.sapiens m
29	305.6	56.6	516	10	HS20162	Z47253 H.sapiens m
30	305.6	56.6	516	10	HS20162	Z47253 H.sapiens m
31	305.6	56.6	527	40	HDWIGHDJA	L23561 Human IGH C
32	304.4	56.4	522	10	HS20269	Z47259 H.sapiens m
33	304.4	56.4	522	10	HS20269	Z47259 H.sapiens m
34	304.4	56.4	522	10	HS20269	Z47259 H.sapiens m
35	304.4	56.4	522	10	HS20269	Z47259 H.sapiens m
36	304	56.3	516	10	HS20161	Z47261 H.sapiens m
37	304	56.3	516	10	HS20161	Z47261 H.sapiens m
38	302	55.9	1553	6	E08434	E08434 CDNA encodl
39	301.4	55.8	525	10	HS20362	Z47269 H.sapiens m
40	301.4	55.8	525	10	HS20362	Z47269 H.sapiens m
41	298.4	55.3	667	6	I65402	I65402 Sequence 1
42	298.4	55.3	803	10	HDWIGHDJA	L22156 Human (clon
43	298.4	55.3	803	10	HDWIGHDJA	L22156 Human (clon
44	298.2	55.2	525	10	HS20361	Z47268 H.sapiens m
45	298.2	55.2	525	40	HS20361	Z47268 H.sapiens m

ALIGNMENTS

RESULT 1						
LOCUS	AR000007	9209 bp	DNA			04-DEC-1998
DEFINITION	Sequence 3 from patent US 5736137.					
ACCESSION	AR000007					
NID	G3962538					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 9209)					
AUTHORS	Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and Rastetter,W.H.					
TITLE	Therapeutic application of chimeric and radiolabeled antilpodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma					
JOURNAL	Patent: US 5736137-A 3 07-APR-1998;					
FEATURES	Location/Qualifiers					
source	1..9209					
BASE COUNT	2239 a 2397 c 2390 g 2183 t					
ORIGIN	/organism="unknown"					

QY	121	TCCAAAGGCTTGGCTACACCTTACACACTACTGATGATGAGGCGGCT	180
Db	169	TCCAAAGCTTCTGGCTACACCTTACACGGCTACTGATACACTGAGTGAAGCAGAGGCT	228
QY	181	GGCCAAAGCTTGTAGATGATGATGAGAGATGATGATCTTCTGAGAGTAATACTACTAACAAT	240
Db	229	GGACAAAGGCTTGTAGATGATGATGAGAGGATTAATCTTACTAGACGGTGTCTGTACTACAAAT	288
QY	241	CAAAATTCGAAGGAGCGCTCACATTGACTGTAGACATTTCCGCTAGCACAGCTCTACATG	300
Db	289	GAGAAGTTCAAACAAAGGACACACTGACTGTAGAACAAATCTCCACACAGCTCTCAAG	348
QY	301	GAGCTCAGAGCGCTGAGATCTGAGAGACACTGCGGGTCTACTATTGTGTCAGAGAGGGGCTAC	360
Db	349	CAACTCAGAGCGCTGACATCTGAGAGACTGTGCGGTATTACTGTGTCAAGAGAGAGGGCC	408
QY	361	GACGATGGGACTATGCTATTGACTACTAGTGGGGTCAAGGACACCTGGTCAACCTGTCTCTCA	420
Db	409	TATGTTTACGAGATGCTATGACTACTGGGGTCAAGGAACCTCAACCGTCTCTCT	468
QY	421	GGCTCACCAGAGGGCCATCGGTCTTCCCGCTGGCACCTCTCTCCAAAGACACTTGGG	480
Db	469	GGCAAAAGCACACCCCATCTGTCTATTCACATGGGCCCTGGATCTGTCTGCCCAAATAAC	528
QY	481	GGCACAGCGGCGCTGGGCTGCTGGTGCAGAGACTACTTCCCGAACCGGTGACGAGTGC	539
Db	529	TCCATGTGTAGACCTTGGAAGGCTGTGTCAGAGGCTATTTCCTGTAGACATGACAGTAC	587
RESULT	4		
LOCUS	164458	1572 bp	DNA
DEFINITION	Sequence 23 from patent US 5665357.	PAT	26-SEP-1997
ACCESSION	164458		
NID	92481352		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1572)		
AUTHORS	Rose, M. Samuel, Boot, C., Copley, C., Graham, Paterson, D. Stephen, Hall, S. Margaret, Wright, A. Firman and Blakey, D. Charles.		
TITLE	Antibodies recognizing tumor associated antigen CA 55.1		
JOURNAL	Patent: US 5665357-A 23 09-SEP-1997;		
FEATURES	location/Qualifiers		
source	1..1572		
BASE COUNT	401 a 465 c 378 g 328 t		
ORIGIN			
Query Match	51.0%;	Score 329.4;	DB 6;
Best Local Similarity	75.7%;	Pred. No. 1.2e-80;	Length 1572;
Matches 408;	Conservative 0;	Mismatches 131;	Indels 0;
Gaps	0;		
QY	1	ATGAATGACACTGGGTCATCTCTCTGTATCAACAGCTACAGCTGCCACCTCCAG	60
Db	49	ATGGATGAGCTATATATCTCTCTTTTGTAGCAACAGTACATATCTCCATCCACG	108
QY	61	GTTCCAACTAGTCACTCTGGGCTGAGGTAAAGAACCTGGGGCTTCACTGAGAGTGTCC	120
Db	109	GTTCCAACTGACACACCTGGGCTGAACTGTGAACCTGGGGCTTCACTGAGAGTGTCC	168
QY	121	TGCAAGGCTTGGCTACACCTTCCACCACTACTGATGATGGGTGAGCGGCGCT	180
Db	169	TGCAAGGCTTGGCTACACCTTCCACCGGCTACTGATACACTGGGTGAAGCAGAGGCT	228
QY	181	GGCCAAAGCTTGTAGATGATGATGAGAGATGATGATCTTCTGAGAGTAATACTACTAACAAT	240
Db	229	GGACAAAGGCTTGTAGATGATGATGAGAGGATTAATCTTACTAGACGGTGTCTGTACTACAAAT	288
QY	241	CAAAATTCGAAGGAGCGCTCACATTGACTGTAGACATTTCCGCTAGCACAGCTCTACATG	300
Db	289	GAGAAGTTCAAACAAAGGACACACTGACTGTAGAACAAATCTCCACACAGCTCTCAAG	348
QY	301	GAGCTCAGAGCGCTGAGATCTGAGAGACACTGCGGGTCTACTATTGTGTCAGAGAGGGGCTAC	360
Db	349	CAACTCAGAGCGCTGACATCTGAGAGACTGTGCGGTATTACTGTGTCAAGAGAGAGGGCC	408
QY	361	GACGATGGGACTATGCTATTGACTACTAGTGGGGTCAAGGACACCTGGTCAACCTGTCTCTCA	420
Db	409	TATGTTTACGAGATGCTATGACTACTGGGGTCAAGGAACCTCAACCGTCTCTCT	468
QY	421	GGCTCACCAGAGGGCCATCGGTCTTCCCGCTGGCACCTCTCTCCAAAGACACTTGGG	480
Db	469	GGCAAAAGCACACCCCATCTGTCTATTCACATGGGCCCTGGATCTGTCTGCCCAAATAAC	528
QY	481	GGCACAGCGGCGCTGGGCTGCTGGTGCAGAGACTACTTCCCGAACCGGTGACGAGTGC	539
Db	529	TCCATGTGTAGACCTTGGAAGGCTGTGTCAGAGGCTATTTCCTGTAGACATGACAGTAC	587

[illegible]

Y	438	ATCGGCTTCCCCCTGGACACCCCTCCGACAGACACTCTGGGGGACACAGGGCCCTGGG	497
Db	453	ATCGGCTTCCCCCTGGACACCCCTCCGACAGACACTCTGGGGGACACAGGGCCCTGGG	512
QY	498	CTGCCTGTCAAGSAGACTTCTCCCGACACGGTGAAGGTCTCG	540
Db	513	CTGCCTGTCAAGSAGACTTCTCCCGACACGGTGAAGGTCTCG	555
RESULT	6		
LOCUS	173104	762 bp	DNA
DEFINITION	Sequence 57 from patent US 5686070.		
ACCESSION	U73104		
NID	93009243		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHOR	1 (bases 1 to 762)		
TITLE	Doerschuk,C.M., Fong,S., Hebert,C.Alice, Kim,K.Jin and Leong,S.R.		
JOURNAL	Methods for treating bacterial pneumonia		
FEATURES	Patent: US 5686070-A 57 11-NOV-1997;		
source	Location/Qualifiers		
	1..762		
	/organism="unknown"		
BASE COUNT	183 a 224 c 186 g 169 t		
ORIGIN			

Query Match	60.7%;	Score 327.8;	DB 6;	Length 762;
Best Local Similarity	78.0%;	Pred. No. 3.3e-80;		
Matches 408; Conservative	0;	Mismatches 112;	Indels 3;	Gaps 1

OY	21	TC	CTCTTG	ATACAAAG	TACAGT	CTCCAT	CCAG	GTCCAACT	AGCAGT	GTG	80
Db	33	TAT	GTCTCTTTTCT	TATGTGTAC	AAACGCGT	AGCTGAGATTTAG	CTGACGAC	GTGTGG			92
OY	81	GCGT	AGGTAAAGAA	GCCTGGGGCT	CTCAGT	AGAGTGTCCG	CAAGGGTCT	TGGCTACAC			140
Db	93	ACCT	AGCTGATGA	AGCCTGGGGCT	TACGT	AAATATCC	TCGCAAGGCT	CTGTGTTATTC			152
OY	141	CTT	CACGACTAG	TGATGCAT	TGGGTGAGG	CAGGCGCGCT	GCCACG	CTTAAGT	GTAT		200
Db	153	ATT	CAGTACCACT	ATCATGCA	CTGGGTGAAC	GACGATGAA	AGAGCCTTGAT	GTGAT			212
OY	201	CGG	AGATGTAT	CTCTTGAG	AGTAACTA	CTACTACAT	AAAAATT	CAAGGACCGT			260
Db	213	TGG	CTACATTAAT	CTTCCAT	TGGTGA	AACTACTTAC	CAACGAAATTC	CAAGGGCAAGGC			272
OY	261	CAC	ATGACTGAG	ACATTTCCG	TAGACAGC	CTACATG	AGTCAAGAC	CCGATATC			320
Db	273	CAC	ATGACTGAG	ACATTTCC	AGACAGC	CCATGTCAT	TCAGAC	CCCTGAATC			322
OY	321	TG	AGACACTCGG	CTACTATT	TGTCAA	AGAGGGGTATG	---	CGACGATGG	ACTATGC		377
Db	333	TG	ATACCTCG	AGCTATTTCT	TGTGCA	AGGGGAGCTAT	GAATG	ATGCAACG	CGACCTGTT		392
OY	378	TAT	TACTACTG	GGGTCAAGG	CAACCTGTG	TACCGTCT	CTCAGC	CTTCAC	CAAGGGCC		437
Db	393	TTT	CGATGCTT	GGGGCGC	GAGGAGCA	CGGTAC	CGTCTCTCC	CTCCAC	CAAGGGCC		452
OY	438	AT	CGGTCTTCCC	CTGGCA	CCCTCTCC	AAAGACCT	CTTGGGGC	CAAGGGCC	CTGGG		497
Db	453	AT	CGGTCTTCCC	CTGGCA	CCCTCTCC	AAAGACCT	CTTGGGGC	CAAGGGCC	CTGGG		512
OY	498	CTG	CGTGGTCA	AGACTACTTCCC	CGAACCGG	TACG	GTGCG				540
Db	513	CTG	CGTGGTCA	AGACTACTTCCC	CGAACCGG	TACG	GTGCG				555

LOCUS	179289	762 bp	DNA	PAT	20-MAR-1998
DEFINITION	Sequence 57 from patent US 5707622.				
ACCESSION	179289				
VERSION	93207579				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 762)				
TITLE	Fong,S.,Hebert,C,Alice, Kim,K.Tin and Leong,S.R.				
JOURNAL	Methods for treating ulcerative colitis				
FEATURES	Patent: US 5707622-A 57 13-JAN-1998;				
SOURCE	Location/Qualifiers				
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BASE COUNT	183 a	224 c	186 g	169 t	
ORIGIN					

Query Match	60.7%;	Score 327.8;	DB 6;	Length 762;
Best Local Similarity	78.0%;	Pred. NO. 3.3e-80;		
Matches 408; Conservative	0;	Mismatches 112;	Indels 3;	Gaps 1

Qy	21	TCCTCTTGGTATCAACAGCTAACAAGTTCACATCTCCAGGTCCAACTAGTCAGTCTGG	80
Db	33	TATGTTCTCTTTTCTTATGCTACAAAACGGGTACGGTGAAGATTGCTGACGACGTTCTGG	92
Qy	81	GCGTAGAGTTAAGAAGCTGGGGGCTTCAGTGAAGGTCTCCGACAGGGTCTGGCTACAC	148
Db	93	ACCTBAGCTGATGAAGCTCGGGGCTTCAGTGAAGATATCTCGCAAGGCTTCTGGTTATTC	152
Qy	141	CTTCACCGACTACTGGATTGCAATTGGGTGAGGCGAGCGCCTGGCCACGTTAGAGTGAT	200
Db	153	ATTGAGTAGCCACATACATGCACTGGGTGAAGACAGGACAGGAAGAAGCCTTGAGTGAT	212
Qy	201	CGAGAGATTGATCTCTTCTGAGAGTAATCTACTACATCAAAAATTCAAGGACCGCT	260
Db	213	TGGCTACATTATATCTTCCATAGTGTGAACACTTACTAACCCAGAAATTCAAGGGCAAGGC	272
Qy	261	CACATTGACTAGACAAATTCGGGTACACAGCCTACATGAGCTCAGCGCCGANAATC	320
Db	273	CACATTGACTGTAGACAAATTCACACACAGCCCAAGCTGCATCTCAGCAAGCCTGACATC	332
Qy	321	TGAGAGCACTCGGCTGTACATTTGTGCAAGGGGGGTTA---CGACGATGGGACTATGC	377
Db	333	TGATGACCTCTGCACTCTATTTCTGTGTGCAAGGGGACTATATGATACACAGGCACTGTT	392
Qy	378	TATTGACTACTGGGGTCAAGGCAACCTGTGTACCGTCTCTCAGCCTTCACCAAGGGCCC	437
Db	393	TTTGATGTCTGGGGCGGAGGACCAAGGTCACGCTCTCCGCGCTTCACCAAGGGCCC	452
Qy	438	ATCGGTCTTCCCCCTGGCACCCTCTCTCCAAAGACACTCTGTGGGGCACAGCGGCTTGGG	497
Db	453	ATCGGTCTTCCCCCTGGGACCCCTCTCTCCAAAGACACTCTGTGGGGCACAGCGGCTTGGG	512
Qy	498	CTGGCTGGTCAAGGACTACTTCCCGGAACGGGTACGGGTGCG	540
Db	513	CTGGCTGGTCAAGGACTACTTCCCGGAACGGGTACGGGTGCG	555

RESULT
I79289

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 762)	Doerschuk, C.M., Fong, S., Hebert, C.Alice, Kim, K.Jin and Leong, S.R	Anti-IL-8 monoclonal antibodies for treatment of inflammatory

disorders
 JOURNAL Patent: US 5702946-A 57 30-DEC-1997;
 FEATURES Location/Qualifiers
 source 1..762
 BASE COUNT 183 a 224 c 186 g 169 t
 ORIGIN

Query Match 60.7%; Score 327.8; DB 6; Length 762;
 Best Local Similarity 78.0%; Pred. No. 3.3e-80;
 Matches 408; Conservative 0; Mismatches 112; Indels 3; Gaps 1;

21 TCTCTCTGTGATCAACAGCTACAGAGTGTCCAGCTCCAGCTACAGTGTGAGTCTGG 80
 33 TAGTTCTGTTTCTTCTATGCTACAAAGCGTACGCTAGATTCACAGCTCAGAGTCTGG 92
 81 GGCTAGGTTAAGAACGCTGGGGCTTCAGTGAAGGTGTCTCCAGAGGGTTCTGGCTACAC 140
 93 ACCTGAGCTGATGAAGCGCTGGGGCTTCAGTGAAGATATCTCCAGAGCTTCTGGTATTC 152
 141 CTTCACCACTACTGGATGATGGGTGAGGAGCGGCTGGCCAGCTCTAGAGTGAT 200
 153 ATTCACTAGCCACTACATCACTGGGTGAGGAGCGGCTGAGAAAGCTTGTAGTGAT 212
 201 CGAGAGATGATGCTTCTGAGAGTATCTACTACTACATCAAAAATTCAGAGGAGCGCT 260
 213 TGGCTACATGATGCTTCTCAATGTAAGTACTACTACTCAACAGAAATTCAGAGGAGCG 272
 261 CACATGAGCTAGACATTTCCGCTAGACACAGCTTACATGAGAGCTCAGAGCTGTGATC 320
 273 CACATGAGCTAGACATTTCCGCTAGACACAGCTTACATGAGAGCTGTGATC 332
 321 TGAGGACACTGGGCTACTATTTGTCAGAGGGGGTAA---CGAGGATGGGACTATAC 377
 333 TATGCTCTGCACTATTTCTGTCAGAGGGGAGCTATGATTAACGGGAGCTGTT 392
 378 TATTGACTAGTGGGCTGAGGACACCTGCTCAGCTCTCTCAGCTCCACCAAGGAGCGCC 437
 393 TTTGATGCTCTGGGGGAGGAGGACAGCTCAACGCTCTCTCGCTCCACCAAGGAGCGCC 452
 438 ATGCGTCTTCCCTGGGACCTCTCTCAAGACACCTCTGGGGGACAGCGGCTCTGG 497
 453 ATGCGTCTTCCCTGGGACCTCTCTCAAGACACCTCTGGGGGACAGCGGCTCTGG 512
 498 CTGCGTGTCAAGAGCTACTTCCCGAAGCGGAGCGGTGTG 540
 513 CTGCGTGTCAAGAGCTACTTCCCGAAGCGGAGCGGTGTG 555

RESULT 9
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 LOCUS Human Igh chain VDJC region mRNA, partial cds.
 DEFINITION L23555
 ACCESSION 949585
 NID
 KEYWORDS C-region; D-region; J-region; V-region; immunoglobulin heavy chain.
 SOURCE Homo sapiens (individual isolate Donor B) adult peripheral blood
 ORGANISM Homo sapiens
 Eukaryote; mitochondria eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 531)
 AUTHORS Chai, S.K., Kasalan, M.T., Ikematsu, H., Kim, M.Y. and Casali, P.
 TITLE VH-D-JH gene sequences of mab produced by human B-1a, B-1b, and B-2
 cells
 JOURNAL Unpublished (1994)
 FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /isolate="Donor B"
 /db_xref="taxon:9606"
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/cell_type="B-cell, EBV-transformed and fused with
 human mouse heterohybridoma F386"
 /dev_stage="adult"
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 /translation="EFMDWTWRIIFLENAATGTHAEVOLVOSGAEVKKPGTTRISK
 VSGYTFDYHMYROAAGKLEWGLVDPEGDAIYPERFOGRTITADSTDAVM
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 BASE COUNT 123 a 152 c 153 g 103 t
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Query Match 60.4%; Score 326.2; DB 10; Length 531;
 Best Local Similarity 77.1%; Pred. No. 8.9e-80;
 Matches 397; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

1 ATGAATGACCTGGGCTATCTCTTGTGATCAACAGCTACAGTGTCCAGTCCAG 60
 9 ATGACTGGACCTGGAGATCCTCTTGTGAGGAGCAGCTACAGGACCCAGCCGAG 68
 61 GTCCAACTAGTCACTTGGGGCTAGGTTAAGAGCTGGGGCTTCAAGTGAAGTGTCC 120
 69 GTCCAACTGGATCTGGGGCTAGGTTAAGAGCTGGGGCTTCAAGTGAAGTGTCC 128
 121 TCCAAAGGTTCTGGCTACACTTCCACAGCTCTGATGATGGGTGAGGAGCGGCT 180
 123 TCCAAAGGTTCTGGCTACACTTCCACAGCTCTGATGATGGGTGAGGAGCGGCT 188
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QY 421 GCCCTCACAGGGCCATGCTTCCCTGACACCTCTCTCAAGACACCTCTGG 480
 DB 429 GCGTCCACCAAGGGCCATGGCTTCCCTGACACCTCTCTCAAGACACCTCTGG 488
 QY 481 GGCACAGCGGCGCTGGCTGCTGCTCAAGACTA 515
 DB 489 GGCACAGCGGCGCTGGCTGCTGCTCAAGACTA 523
 RESULT 10
 HUMIGHDUA 531 bp mRNA PRI 09-NOV-1994
 LOCUS Human IGH chain VDJC region mRNA, partial cds.
 DEFINITION L23555
 ACCESSION 9499585
 NID C-region; D-region; J-region; V-region; Immunoglobulin heavy chain.
 KEYWORDS Homo sapiens (Individual isolate Donor B) adult peripheral blood
 SOURCE CDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 531)
 Chai, S.K., Kasalan, M.T., Ikematsu, H., Kim, M.Y. and Casali, P.
 VH-D-JH gene sequences of mab produced by human B-1a, B-1b, and B-2 cells
 JOURNAL Unpublished (1994)
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 /dev_stage="adult"
 /tissue_type="peripheral blood"
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 429..531
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 BASE COUNT 123 a 152 c 153 g 103 t
 ORIGIN

Query Match 60.4%; Score 326.2; DB 40; Length 531;
 Best local similarity 77.1%; Pred. No. 8.9e-80;
 Matches 397; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
 QY 1 ATGAAATGACCTGGGTCTCTCTTCTGATCAACAGCTACAGAGTGTCCAG 60
 DB 9 ATGAGCTGACCTGGAGATTCCTCTTGGAGGACAGCTACAGGACCCAGCGAG 68
 QY 61 GTCCACTAGTGTGAGCTGGGCTGAGTTAAGAGCCGCGGCTCATAGAGTGTCC 120
 DB 69 GTCCAACTGTATAGTCTGGGCTGAGTGAAGAACCTGGGACTACAGTGAATCTCC 128
 QY 121 TGCAGAGTTCTGGCTACACCTTACACCTAGTGTGATGGGTGAGGAGCGCCT 180
 DB 129 TGCAGAGTTCTGGATACACCTTACACCTAGTGTGATGGGTGAGGAGCGCCT 188
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 DB 189 GGAAGAGGCTTGAAGTGGGCTGAGTGTGATCTTGAAGAGTGAAGCAATCTACCA 248
 QY 241 CAAATTCAGAGGACCGCTACATTTGATGACATTTCCGCTACAGCCTACATG 300
 DB 249 GAGAAATTCAGAGGACCGCTACATTTGATGACATTTCCGCTACAGCCTACATG 308
 QY 301 GAGCTACAGCCTGAGATCTGAGACACTGGGCTCTACTATTGTCAGAGGAGGTAC 360
 DB 309 GAGGTACAGCCTGAGATCTGAGACACTGGGCTCTACTATTGTCAGAGGAGGTAC 368
 QY 361 GACGATGGGACTATGATCTGATGACAGGACCGCTGCTACCGCTCTCTCA 420
 DB 369 AATATATCCCGCCACCGGTATGACGCTGGGCGCAAGGAGACCGCTACCGCTCTCA 428
 QY 421 GCGTCCACCAAGGCGCCATCGCTTCCCTGCGACCCCTCTCTCAAGAGCACTCTGG 480
 DB 429 GCGTCCACCAAGGCGCCATCGCTTCCCTGCGACCCCTCTCTCAAGAGCACTCTGG 488
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 DB 489 GGCACAGCGGCGCTGGCTGCTGCTGCTCAAGACTA 523
 RESULT 11
 MUSIGH1H 1544 bp mRNA ROD 25-APR-1996
 LOCUS Mouse mRNA for immunoglobulin gamma-3 V-D-J region and secreted
 DEFINITION constant region, complete cds.
 ACCESSION D14625
 NID 9286089
 KEYWORDS Immunoglobulin gamma-3 secreted C-region; Immunoglobulin V region;
 immunoglobulin gamma-3 heavy chain; Immunoglobulin gamma-3 heavy
 chain precursor.
 SOURCE Mus musculus (strain: MRL/MPJ-lpr/lpr, library: pBluescript KS(+))
 adult CDNA to mRNA, clone pB1H1.
 ORGANISM Mus musculus
 Eukaryota; Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Euthera; Rodentia; Soturognathi; Muridae;
 Murinae; Mus.
 1 (bases 1 to 1544)
 Takahashi, S., Itoh, D., Nose, M., Ono, M., Yamamoto, T. and Kyogoku, M.
 Cloning and cDNA sequence analysis of nephritic monoclonal
 antibodies derived from an MRL/lpr lupus mouse
 JOURNAL Mol. Immunol. 30 (2), 177-182 (1993)
 MEDLINE 93156722
 REFERENCE 2 (sites)
 AUTHORS Ono, M., Yamamoto, T., Kyogoku, M. and Nose, M.
 TITLE Sequence analysis of the germ-line VH gene corresponding to a
 nephritic antibody in MRL/lpr lupus mice
 JOURNAL Clin. Exp. Immunol. 100 (2), 284-290 (1995)
 MEDLINE 95262286
 REFERENCE 3 (bases 1 to 1544)
 AUTHORS Nose, M.

TITLE Direct Submission
JOURNAL Submitted (10-MAR-1993) to the DDBJ/EMBL/Genbank databases...Masato Nose, Tohoku University School of Medicine, Dept. of Pathology; 2-1 Seiry-cho Aoba-ku, Sendai, Miyagi-ken 980, Japan (E-mail: d22181@ccu.cc.tohoku.ac.jp, Tel: 022-273-9042, Fax: 022-234-1986)
COMMENT Submitted (10-MAR-1993) to DDBJ by: Nose Masato
 Dept. of Pathology
 Tohoku University School of Medicine
 2-1 Seiry-cho
 Aoba-ku
 Sendai
 Miyagi 980
 Japan
 Phone: 022-273-9042
 Fax: 022-234-1986
 Email: d22181@ccu.cc.tohoku.ac.jp.
FEATURES
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 Best Local Similarity 75.4%; Pred. No. 2.2e-79;

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 QY 241 CAAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 Db 273 GAGAAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 332
 QY 301 GAGCTAGACGCTGATGATCTGAGACACTGCGGTCTACTATTGCAAGAGGGGTAC 360
 Db 333 CAGCTAGACGCTGATGATCTGAGACACTGCGGTCTACTATTGCAAGAGGGGTAC 392
 QY 361 GAGCATGGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 393 GGGGAGTATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 452
 QY 421 GCCTCCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
 Db 453 GCTACCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 512
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 Db 513 TCCTCGTGACACTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 568
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HUMIGHBPAN LOCUS 1599 bp mRNA 08-OCT-1993
DEFINITION Human (hybridoma H210) anti-hepatitis A IgG variable region,
 constant region, complementarily-determining regions mRNA, complete
 cds.
ACCESSION M87789
KEYWORDS 9185361
 complementarity-determining region; constant region; Immunoglobulin
 gamma-chain; Immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens
 Homo sapiens cDNA to mRNA.
ORGANISM Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1599)
 Lewis, A.P., Lemon, S.M., Barber, K.A., Murphy, P., Parry, N.R.,
 Peakman, T.C., Sims, M.J., Worden, J., and Crowe, J.S.
 Rescue, expression, and analysis of a neutralizing human
 anti-hepatitis A virus monoclonal antibody
 J. Immunol. 151 (5), 2829-2838 (1993)
JOURNAL 93367243
MEDLINE
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Matches 421; Conservative 0; Mismatches 119; Indels 18; Gaps 1;

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QY 61 GTCCAACTAGTGCAGCTGGGGCTGAGGTTAAGAAGCTGGGGCTTCAGTGAAGTGTCC 120
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QY 181 GGCACAGCTCAGAGTGGATGGAGAGATTATCTTCTGAGAGTAACTACTACTAAT 240
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Matches 421; Conservative 0; Mismatches 119; Indels 18; Gaps 1;

QY 1 ATGAATGCACTGGGCTATCTTCTTGTATCAACAGTACAAAGTTCACCTCCAG 60
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RESULT 14

LOCUS 158595 3282 bp DNA PAT 14-AUG-1997
DEFINITION Sequence 154 from patent US 5652138.
ACCESSION 158595
NID 92477833
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3282)
AUTHORS Burton,D.R., Barbas,C.F. and Lerner,R.A.
TITLE Human neutralizing monoclonal antibodies to human immunodeficiency virus

JOURNAL Patent: US 5652138-A 154 29-JUL-1997;

FEATURES
source 1.3282 Location/Qualifiers

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ORIGIN

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Best Local Similarity 75.1%; Pred. No. 1.3e-77;
Matches 419; Conservative 0; Mismatches 121; Indels 18; Gaps 1;

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DB 75 GTTCAAGTGTGCAAGTGTGGGCTGAGGTTAAGAGAGCTGGGCTTGAAGTGTCC 134
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DB 135 TGTAGAGCTTGTGATACAGTATCAAGTATGATTTGATGATGGGTGAGCAGGCT 194
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LOCUS 158596 13254 bp DNA PAT 14-AUG-1997
DEFINITION Sequence 156 from patent US 5652138.
ACCESSION 158596
NID 92477834
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13254)
AUTHORS Burton,D.R., Barbas,C.F. and Lerner,R.A.
TITLE Human neutralizing monoclonal antibodies to human immunodeficiency virus

JOURNAL Patent: US 5652138-A 156 29-JUL-1997;

FEATURES
source 1.13254 Location/Qualifiers

BASE COUNT 3206 a 3559 c 3251 g 3238 t

ORIGIN

Query Match 59.0%; Score 318.4; DB 6; Length 13254;
Best Local Similarity 75.1%; Pred. No. 1.4e-77;
Matches 419; Conservative 0; Mismatches 121; Indels 18; Gaps 1;
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Job time: 1480 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 11:44:14 ; Search time 479.58 Seconds
(without alignments)
1/17.605 Million cell updates/sec

Title: US-08-700-737-18

Perfect score: 540
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Scoring table: IDENTITY_NUC

Searched: 2002476 seqs, 762712212 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	184.6	34.2	432	31	AI268604	AI268604
	5	180.4	33.4	294	28	AI007196	AI007196
	6	170.2	31.5	256	17	AA300605	AA300605
	7	157.8	29.2	437	13	HS053086	HS053086
	8	157.4	29.1	279	17	AA300571	AA300571
	9	152	28.1	366	19	AA378312	AA378312
	10	152	28.1	366	29	AA987559	AA987559
	11	148.4	27.5	379	21	AA291381	AA291381
	12	148.4	27.5	431	25	AA710970	AA710970
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	18	137	25.2	265	18	AA377128	AA377128
	19	136.2	25.2	199	12	H61366	H61366
	20	135.6	25.1	267	18	AA360197	AA360197
	21	131.6	24.4	346	13	HS053085	HS053085
	22	123.2	22.8	266	24	AA402547	AA402547
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	27	115	21.3	372	25	AA581192	AA581192
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	29	112	20.7	230	18	AA346313	AA346313
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	31	104.2	19.3	378	26	AA740786	AA740786
	32	102.6	19.0	319	23	AI299479	AI299479
	33	101	18.7	271	18	AA369101	AA369101
	34	100.6	18.6	630	27	AA895088	AA895088
	35	100.4	18.3	438	24	AA622457	AA622457
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	37	98.6	18.3	419	12	H73816	H73816
	38	96.6	17.9	238	21	AA505044	AA505044
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	40	91	16.9	485	29	AA988730	AA988730
	41	89.2	16.5	430	11	R72787	R72787
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	43	84	15.6	304	17	AA300945	AA300945
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ALIGNMENTS

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Similar to gb:L02325 IG HEAVY CHAIN PRECURSOR V-1 REGION (HUMAN).
mRNA sequence.
ACCESSION AA569186
NID 92342240
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLB at:
www-bio.lnl.gov/db/brp/image/image.html

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FEATURES

Location/Qualifiers

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 Reference: Krizman et al. (1996) Cancer Research
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 OY 61 GTCCACTAGTACAGTCTGGGCTGAGTTAAGAAAGCTGGGGCTTCACTGAAGTCTCC 120
 DB 98 GTCCAACTGCTGACATCTGGGCTGAGTGAAGAACCCGGGCTTCACTGAAGTCTCC 157
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 DB 158 TGTAAAGCTCTGATGATCCCTCCACCACTGATGATGGGTGGAGGCGCT 217
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 OY 241 CAAAATTCAGGAGCGCTCACATTTGATGATTCCTTCTGAGAGTAACTACTACTACAT 300
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 DB 338 GAGCTCAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 387

RESULT 2

LOCUS A1180569 310 bp mRNA EST 08-OCT-1998
 DEFINITION uc00f09.r1 Soares mouse mammary gland NbMNG Mus musculus CDNA clone
 1431017 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION
 (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene
 mRNA; complete (MOUSE); mRNA sequence.

ACCESSION

A1180569

NID

93731207

KEYWORDS

EST.

ORGANISM

house mouse.

REFERENCE

1 (bases 1 to 310)
 Rodentia; Scleroglossa; Muridae; Murinae; Mus.
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubaque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

TITLE
 JOURNAL
 COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNLB; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:915085
 Seq primer: -28m13 rev2 Err from Amersham.

FEATURES

Location/Qualifiers

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 /strain="C57BL/6J"
 /note="Organ: mammary gland; Vector: pT7T3D-Pac
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 T 3'); double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT7T3 vector.
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
 constructed and normalized by Bento Soares and M. Fatima
 Bonaldo."
 /db_xref="taxon:10090"
 /clone="1431017"
 /clone_lib="Soares mouse mammary gland NbMNG"
 /sex="male"
 /tissue_type="mammary gland"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 BASE COUNT 80 a 77 c 85 g 67 t 1 others
 ORIGIN

Query Match 37.3% Score 201.4; DB 30; Length 310;
 Best Local Similarity 83.9%; Pred. No. 7.3e-50;
 Matches 251; Conservative 0; Mismatches 46; Indels 2; Gaps 2;

OY 58 CAGTCCACTAGTACAGTCTGGGCTGAGTTAAGAGCCTGGGGCTTCACTGAAGTG 117
 DB 1 CAGTCCACTAGTACAGTCTGGGCTGAGTTAAGAGCCTGGGGCTTCACTGAAGTG 58
 OY 118 TCCGCAAGGCTTGGGCTACACCTTCCACGACTGATGATGATGATGATGATGATG 177
 DB 59 TCCGCAAGGCTTGGGCTACACCTTCCACGACTGATGATGATGATGATGATGATG 118
 OY 178 CCTGCAACGCTAGTGTGATCGAGAGATGATCTTCTGAGAGTAACTACTACTAC 237
 DB 119 CCGTGAACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 178
 OY 238 AATCAAAATTCAGGAGCGCTCACATTTGATGATGATGATGATGATGATGATGATG 297
 DB 179 AATCAAAATTCAGGAGCGCTCACATTTGATGATGATGATGATGATGATGATGATG 238
 OY 298 ATGAGGCTCAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 356
 DB 239 ATGAGGCTCAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 297

RESULT 3

LOCUS A1201426/c 461 bp mRNA EST 30-OCT-1998
 DEFINITION qs73c06.x1 NCI CGAP Pr28 Homo sapiens CDNA clone IMAGE:1943722 3'
 similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION

ACCESSION	ORGANISM	REFERENCE	COMMENT
NID	human.	1 (bases 1 to 461)	Unpublished (1997)
KEYWORDS	Human sapiens	1 (bases 1 to 461)	Unpublished (1997)
SOURCE	Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	1 (bases 1 to 461)	Unpublished (1997)
REFERENCE	Primates; Catarrhini; Hominiidae; Homo.	1 (bases 1 to 461)	Unpublished (1997)
AUTHORS	NCI-CGAP	1 (bases 1 to 461)	Unpublished (1997)
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	1 (bases 1 to 461)	Unpublished (1997)
JOURNAL	Tumor Gene Index	1 (bases 1 to 461)	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.	1 (bases 1 to 461)	Unpublished (1997)
FEATURES	Tel: (301) 496-1550	1 (bases 1 to 461)	Unpublished (1997)
source	Email: Robert.Strausberg@nih.gov	1 (bases 1 to 461)	Unpublished (1997)
	unknown library type	1 (bases 1 to 461)	Unpublished (1997)
	Insert length: 608 Std Error: 0.00	1 (bases 1 to 461)	Unpublished (1997)
	Seq primer: -400P from Glbco.	1 (bases 1 to 461)	Unpublished (1997)
	Location/Qualifiers	1 (bases 1 to 461)	Unpublished (1997)
	1. 461	1 (bases 1 to 461)	Unpublished (1997)
	/organism="Homo sapiens"	1 (bases 1 to 461)	Unpublished (1997)
	/note="Organ: prostate; Vector: PT7r3d-Pac (Pharmacia)	1 (bases 1 to 461)	Unpublished (1997)
	with a modified polylinker: plasmid DNA from the	1 (bases 1 to 461)	Unpublished (1997)
	normalized library NCI-CGAP_Pr22 was prepared, and s	1 (bases 1 to 461)	Unpublished (1997)
	clones were made in vitro. Following RAP purification,	1 (bases 1 to 461)	Unpublished (1997)
	this DNA was used as tracer in a subtractive hybridization	1 (bases 1 to 461)	Unpublished (1997)
	reaction. The driver was PCR-amplified cDNAs from a pool	1 (bases 1 to 461)	Unpublished (1997)
	of 5,000 clones made from the same library (clonoids	1 (bases 1 to 461)	Unpublished (1997)
	98508-986759, 1101192-1101959, and 1217928-1220615).	1 (bases 1 to 461)	Unpublished (1997)
	Subtraction by Bento Soares and W. Fatima Bonaldi."	1 (bases 1 to 461)	Unpublished (1997)
	/db_xref="taxon:9606"	1 (bases 1 to 461)	Unpublished (1997)
	/clone="IMAGE:1943722"	1 (bases 1 to 461)	Unpublished (1997)
	/clone_1lb="NCI-CGAP_Pr28"	1 (bases 1 to 461)	Unpublished (1997)
	/sex="male"	1 (bases 1 to 461)	Unpublished (1997)
	/dex_stage="adult"	1 (bases 1 to 461)	Unpublished (1997)
	/lab_host="DH10B"	1 (bases 1 to 461)	Unpublished (1997)
	/lab="lab"	1 (bases 1 to 461)	Unpublished (1997)
BASE COUNT	93 a 132 c 106 g 130 t	1 (bases 1 to 461)	Unpublished (1997)
ORIGIN		1 (bases 1 to 461)	Unpublished (1997)
Query Match	36.7%; Score 198; DB 31; Length 461;	1 (bases 1 to 461)	Unpublished (1997)
Best Local Similarity	76.4%; Pred. No. 8.3e-49;	1 (bases 1 to 461)	Unpublished (1997)
Matches 243; Conservative	0; Mismatches 75; Indels 0; Gaps 0;	1 (bases 1 to 461)	Unpublished (1997)
35	CAACAGCTACAGAGTCCACTCCAGGTCACAACTAGTCAGTCGGGGCTGAGGTTAAGA 94	1 (bases 1 to 461)	Unpublished (1997)
461	CACCAAGCTACAGAGTCCACTCCAGGTCACAACTAGTCAGTCGGGGCTGAGGTTAAGA 402	1 (bases 1 to 461)	Unpublished (1997)
95	AGCCTGGGGCTTACAGTGAAGGTGTCCTCAAGAGGTTCTGGCTACACCTTCCACAGTACT 154	1 (bases 1 to 461)	Unpublished (1997)
401	AGCCTGGGGCTTACAGTGAAGGTGTCCTCAAGAGGTTCTGGCTACACCTTCCACAGTACT 342	1 (bases 1 to 461)	Unpublished (1997)
155	GGATGTCAGTGGGTGAGCAGGCGCTGGCCAAAGCTCTAGAGTGGATCGGAGAGATTGATC. 214	1 (bases 1 to 461)	Unpublished (1997)
341	ATATGCTACTGGGTGGAGCAGGCGCTGGCCAAAGAGCTTGGGTGGATGGAGCGGATCAACC 282	1 (bases 1 to 461)	Unpublished (1997)
215	CTTCTGAGAGTAATCTACTACATCAAAATTCAAAGAGCGGCTGCATTTGACTAG 274	1 (bases 1 to 461)	Unpublished (1997)
281	CTAACAGTGGTGGCCAAAGCTATGTCACGAAAGTTCCAGGAGGAGAGTCCATTCACCAAGG 222	1 (bases 1 to 461)	Unpublished (1997)
275	ACATTTCCGCTAGCAGCAGCTTACATGAGTCAAGAGCTGAGATCTGAGAGACCTGGG 334	1 (bases 1 to 461)	Unpublished (1997)
221	ACAGCTCATCAGCAGCAGCTTACATGAGTCAAGAGCTGAGAGCTGAGATCTGAGAGACCGGCA 162	1 (bases 1 to 461)	Unpublished (1997)
335	TCCTACTATTTGTCAGAG 352	1 (bases 1 to 461)	Unpublished (1997)
161	CGTATTACTGTGGCAGAG 144	1 (bases 1 to 461)	Unpublished (1997)

LOCUS	AI268604	432 bp	mRNA	EST	17-NOV-1998
DEFINITION	9c47a10.x1 NCI CGAP Llus Homo sapiens cDNA clone IMAGE:1911642 3'				
ACCESSION	AI268604				
NID	93887771				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
AUTHORS	Primates; Catarrhini; Homidae; Homo.				
TITLE	1 (bases 1 to 432)				
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)				
FEATURES	Source				
FEATURES	Seq primer: -40UP from G1bco High quality sequence stop: 409.				
FEATURES	Location/Qualifiers				
FEATURES	1. .432				
FEATURES	/organism="Homo sapiens"				
FEATURES	/note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p703 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."				
FEATURES	/db_xref="taxon:9606"				
FEATURES	/clone="IMAGE:1911642"				
FEATURES	/clone_1lb="NCI CGAP Llus"				
FEATURES	/tissue_type="carcinoid"				
FEATURES	/lab_host="DH10B"				
FEATURES	/lab_host="DH10B"				
BASE COUNT	92 a 122 c 127 g 91 t				
ORIGIN					
Query Match	34.2% Score 184.6; DB 31; Length 432;				
Best Local Similarity	65.7% Pred. No. 7.7e-45;				
Matches 287; Conservative 0; Mismatches 144; Indels 6; Gaps 1;					
43 ACAAGTCCACATCCACAGTCCCACTAGTGTGGGGTGAAGGCTTGAAGAGCCTGGG 102					
2 AAAGTGTCCAGTGTGAGAGTGTGAGTGTGAGTGTGGGGGAGAGTGTGTCAGCCTGGG 61					
103 GCTTCAGTGAAGGTGTCTGCAAGGGTTCGTGCTACACCTTCACCGACTACTGATGCAT 162					
62 GGGTCCCTGAGACTCTCTGTCGACACCTGTGATTCATCTTAGACGATATGCCATGAAC 121					
163 TGGGTGAGGCAAGGCGCTGGGCCAACGCTTAGAGTGTGATCGGAGAGATGTATCTTCTGAG 222					
122 TGGGTCCCGGAGGCTCCAGGGAAGGGGCTGAGTGTGCTCATTTGTTAAATTAACGTTGGG 181					
223 AGTAATACTACTACTAATCAAAAATTCAGAGGAGCGCACATTTAGCTGTGACATTTCC 282					
182 ACTCAAAACACACGACGACACTCCGTGAAGGGCCGTTTATCATCTCCAGAGACAAATTC 241					
283 GCTAGCACAGGCTCATGATGAGAGCTGACGACCTGATGATCTGAGACACTGCGTCTACTAT 342					

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression

Query Match 27.1%; Score 146.4; DB 11; Length 287; Best Local Similarity 73.2%; Pred. No. 1.5e-33; Matches 186; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 ATGATGACACCTGGGCTATCTCTTGTGATCAACAGCTACAGTCCACTCCAG 60
 DB 14 ATGACAGGACCTGAGATCTCTTGTGATGACAGCAGCAGCAGCAGCAGCAG 73
 QY 61 GTCCACTAGTGTGAGTGGGGCTGAGTTAAGAGCTGGGGCTGAGTGAAGGTCC 120
 DB 74 GTCCACTAGTGTGAGTGGGGCTGAGTTAAGAGCTGGGGCTGAGTGAAGGTCC 133
 QY 121 TGCACAGGCTGTGAGTGGGGCTGAGTTAAGAGCTGGGGCTGAGTGAAGGTCC 180
 DB 134 TGCACAGGCTGTGAGTGGGGCTGAGTTAAGAGCTGGGGCTGAGTGAAGGTCC 193
 QY 181 GGCACAGGCTGTGAGTGGGGCTGAGTTAAGAGCTGGGGCTGAGTGAAGGTCC 240
 DB 194 GGCACAGGCTGTGAGTGGGGCTGAGTTAAGAGCTGGGGCTGAGTGAAGGTCC 253
 QY 241 CAAATATTCAGAGG 254
 DB 254 CAAATATTCAGAGG 267

RESULT 14

H68593 223 bp mRNA EST 27-OCT-1995
 LOCUS H68593
 DEFINITION yu69606.r1 Homo sapiens cDNA clone 239074 5' similar to gb:M87789
 IG GAMA-1 CHAIN C REGION (HUMAN);

ACCESSION H68593
 NID 91027333

KEYWORDS EST.

ORGANISM human clone-239074 primer-M13R1 library-Weismann Olfactory
 Epithelium vector-pBluescript SK- host-SOUR cells (kanamycin
 resistant) Rsite1-ECORI Rsite2-XhoI From 35 year old female. The
 cDNA was oligo (dT) primed with an XhoI restriction enzyme
 recognition site and an 18 base poly dT sequence. For the 5' end,
 the synthesized cDNA termini were treated with T4 DNA polymerase
 and EcoRI adaptors were ligated to the blunt ends.

REFERENCE Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 223)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Matra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasaks, E.,
 Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 WashU-Merck EST project
 Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Source: IMAGE Consortium, LBNL
 This clone is available royalty-free through LBNL; contact the
 IMAGE Consortium (info@image.lbnl.gov) for further information.
 Location/Qualifiers

FEATURES

source

1. 223

/organism="Homo sapiens"

/clone="239074"

<1. >223

35 a 75 c 66 g 46 t 1 others

BASE COUNT

ORIGIN

Query Match 26.7%; Score 144; DB 12; Length 223; Best Local Similarity 93.2%; Pred. No. 7.2e-33; Matches 150; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 376 GCTATGACACTGGGGCTAAGCAGCAGTGTACCGTCTCCACAGTCCAGAGGGC 435
 DB 60 GCTTGGACCCCTGGGGCCAGGAGACCTGTCTCCGTCTCCACAGTCCAGAGGGC 119
 QY 436 CCATGGCTTCCCTGGGACCCCTCTCCAGAGCAGCAGTGGGGGACAGGGCCCTG 495
 DB 120 CCATGGCTTCCCTGGGACCCCTCTCCAGAGCAGCAGTGGGGGACAGGGCCCTG 179
 QY 496 GGCTGCTGTGCAAGGACTACTTCCCGAACCAGCGTACCGT 536
 DB 180 GGCTGCTGTGCAAGGACTACTTCCCGAACCAGCGTACCGT 220

RESULT 15

AA377074 291 bp mRNA EST 21-APR-1997
 LOCUS AA377074
 DEFINITION EST89603 Small intestine I Homo sapiens cDNA 5' end similar to
 similar to immunoglobulin heavy chain, VDJ regions (GB:214165),
 mRNA sequence.

ACCESSION AA377074

NID 92029413

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryotes; mitochondria eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
 Homo.
 1 (bases 1 to 291)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fullmer, R.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, Wai, C.,
 Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marnaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, O.L., Sauder, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Yi, Y.,
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
 Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
 Fraser, C.M. and Venter, J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (http://www.tigr.org/db/hgi/hgi.html)
 Seq primer: M13 Reverse.
 Location/Qualifiers

FEATURES

source

1. 291

/organism="Homo sapiens"

/note="Organ: small intestine; Vector: pBluescript SK-;

Site_1: ECORI; Site_2: XhoI"

/db_xref="ATCC (inhost):181500"

/db_xref="taxon:9606"

/clone_lib="Small intestine I"

GenCore version 4.5
(c) 1993 - 1998 CompuLink

ALIGNMENTS

(without alignments)
1147.790 Million cell updates/sec

CCGACC GGTCG 540

predicted by chance to have a score of the result being printed, the actual score distribution.

LES

Accession	Description
U00096	DNA encoding the h
U00097	Consensus DNA sequ
U00098	DNA encoding murin
U00099	Vector contg. TCAR
U00100	DNA sequence of m
U00101	Chimeric heavy cha
U00102	2A2 (Chimeric) hu
U00103	Murine anti-porcini
U00104	2A2 human g2/g4 c
U00105	2A2 human IgG4 exp
U00106	Murine anti-porcini
U00107	3F4 (Chimeric) hu
U00108	3F4 human g2/g4 c
U00109	3F4 human IgG4 exp
U00110	Plasmid pAH4602. A
U00111	Mab 55.1 heavy cha
U00112	Anti-IL-8 Mab 6G4
U00113	Chimeric monoclonal
U00114	Chimeric monoclonal
U00115	Murine variable re
U00116	Chimeric monoclonal
U00117	Chimeric Mab 6G4.2
U00118	Plasmid pAH4625. A
U00119	Antibody D heavy c
U00120	Humanised 5G1.1 VH
U00121	Plasmid pAH4808. A
U00122	Humanised 5G1.1 VH
U00123	OKT3 monoclonal an
U00124	Anti-tobacco mosai
U00125	VH186 region of an
U00126	PCmb3 expression
U00127	Expression vector
U00128	PC3A9J31 anti-teta
U00129	Encodes 4D5 Fab Ig
U00130	Reshaped CD4 antiI
U00131	Reshaped CD4 antiI
U00132	Reshaped CAMPAT-1
U00133	Approximate nucle

Query Match	100.0%	Score 540:	DB 1:	Length 540:
Best Local Similarity	100.0%	Pred. No. 8e-132:		
Matches 540:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
1 ATGAATGACACCTGGGCTATCTCTCTTGGTATCAACAGCTACAAAGTGTCCACCTCCAG 60				
1 ATGAATGACACCTGGGCTATCTCTCTTGGTATCAACAGCTACAAAGTGTCCACCTCCAG 60				
61 GTTCAACATGAGTGTGGGCTGAGGCTTAAGAAAGCTGGGGCTTCAAGTGAAGGTGCC 120				
61 GTTCAACATGAGTGTGGGCTGAGGCTTAAGAAAGCTGGGGCTTCAAGTGAAGGTGCC 120				
61 GTTCAACATGAGTGTGGGCTGAGGCTTAAGAAAGCTGGGGCTTCAAGTGAAGGTGCC 120				
121 TGCAGGGTTGTGGCTACCTTCCACAGCTACTGATGATGATGGGTGAGGACGCGCT 180				
121 TGCAGGGTTGTGGCTACCTTCCACAGCTACTGATGATGATGGGTGAGGACGCGCT 180				
121 TGCAGGGTTGTGGCTACCTTCCACAGCTACTGATGATGATGGGTGAGGACGCGCT 180				

QY 181 GCCCAAGCTCTAGAGTGTGATGAGAGATGATCTCTCTGAGAGTAACTACTACAT 240
 CC using degenerate PCR primers V20079-82. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 494 BP; 113 A; 120 C; 118 G; 104 T;

QY 361 GACGATGGAGCTAATGCTATTGCTACTGAGGCTCAAGGACCTGTCACCTCTCTCA 420
 DB 361 GACGATGGAGCTAATGCTATTGCTACTGAGGCTCAAGGACCTGTCACCTCTCTCA 420
 QY 421 GCCCTCCACCAAGGCCATTCGCTCTCCCTGACACCTCTCTCCAAAGACCTCTGG 480
 DB 421 GCCCTCCACCAAGGCCATTCGCTCTCCCTGACACCTCTCTCCAAAGACCTCTGG 480
 QY 481 GGCACAGCGGCTGGGCTGCTGGTCAAGGACTACTCTCCGGAACGGTGACGGTCTG 540
 DB 481 GGCACAGCGGCTGGGCTGCTGGTCAAGGACTACTCTCCGGAACGGTGACGGTCTG 540

RESULT 2

V20085
 ID V20085 standard; DNA; 494 BP.

AC 14-JUL-1998 (first entry)
 DE Consensus DNA sequence of the murine variable heavy chain region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease; ss.
 OS Mus sp.

FT Key
 FT CDS

Location/Qualifiers
 13..445
 /tag- a
 /note- "no stop codon given"
 /transl_except- (pos: 16..18, aa: Xaa)
 /transl_except- (pos: 19..21, aa: Xaa)
 /transl_except- (pos: 22..24, aa: Xaa)
 /transl_except- (pos: 25..27, aa: Xaa)
 /transl_except- (pos: 28..30, aa: Xaa)
 /transl_except- (pos: 31..33, aa: Ile)
 /transl_except- (pos: 34..36, aa: Xaa)
 /note- "Xaa- unknown"
 13..69
 /tag- d
 /tag- e

FT sig_peptide
 FT mat_peptide

70..445
 /tag- e

NO9806248-A2.

PD 19-FEB-1998.
 PR 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J.
 DR WPL; 98-159172/14.
 DR P-PSDB; W53816.
 PT Humanised immunoglobulin reactive with alpha4-beta7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 1; 145pp; English.
 CC The present sequence represents the consensus nucleotide sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse heavy chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal adressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in muscosal

CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20079-82. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 494 BP; 113 A; 120 C; 118 G; 104 T;

Query Match

Best Local Similarity 83.0%; Pred. No. 3,7e-90;
 Matches 399; Conservative 23; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATGAATGACACCTGGGCTATCTCTTCTGATCAACAGCTACAGTCTCCAG 60
 DB 13 ATGRRATGASCTRRKATATCTCTTCTGATCAACAGCTACAGTCTCCAG 72
 QY 61 GTCCAACTAGTACAGTCTGGGCTGAGGCTTAAGAGGCTGGGCTTCAAGAGTCTCC 120
 DB 73 GTCCAACTAGTACAGTCTGGGCTGAGGCTTGAAGGCTTGAAGAGTCTCTCC 132
 QY 121 TGCAAGGATCTGCTACACCTTCAACAGCTACAGTCTGAGGCTGAGGAGGCTCT 180
 DB 133 TGCAAGGATCTGCTACACCTTCAACAGCTACAGTCTGAGGCTGAGGAGGCTCT 192
 QY 181 GGCACAGCTCTAGAGTGTGATGAGAGATGATCTCTGAGAGTAACTACTACAT 240
 DB 193 GGCACAGCTCTAGAGTGTGATGAGAGATGATCTCTGAGAGTAACTACTACAT 252
 QY 241 CAAATATCAAGGAGGAGCGCTACATCTGATGAGATCTCTGATGAGATCTGATGAG 300
 DB 253 CAAATATCAAGGAGGAGCGCTACATCTGATGAGATCTCTGATGAGATCTGATGAG 312
 QY 301 GAGCTCAGACCTGAGATCTGAGAGACATGCGGCTCTACTATTGTGCAAGAGGGGTTAC 360
 DB 313 GAGCTCAGACCTGAGATCTGAGAGACATGCGGCTCTACTATTGTGCAAGAGGGGTTAC 372
 QY 361 GACGATGGAGCTAATGCTATTGCTACTGAGGCTCAAGGACCTGTCACCTCTCTCA 420
 DB 373 GACGATGGAGCTAATGCTATTGCTACTGAGGCTCAAGGACCTGTCACCTCTCTCA 432
 QY 421 GCCCTCCACCAAGGCCATTCGCTCTCCCTGACACCTCTCTCCAAAGACCTCTGG 480
 DB 433 GCCCTCCACCAAGGCCATTCGCTCTCCCTGACACCTCTCTCCAAAGACCTCTGG 492
 QY 481 G 481
 DB 493 G 493

RESULT 3

V20078
 ID V20078 standard; DNA; 420 BP.

AC 14-JUL-1998 (first entry)
 DE DNA encoding murine Act-1 heavy chain variable region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease; ss.
 OS Mus sp.

FT Key
 FT CDS

Location/Qualifiers
 1..420
 /tag- a
 /tag- b

FT sig_peptide
 FT mat_peptide

1..57
 /tag- b

58..420

FT sig_peptide
 FT mat_peptide

FT /tag- C
 PN WO9806248-A2.
 PD 19-FEB-1998.
 PE 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Salama J.
 DR WPI: 98-159172/14.
 P-PDB: W53815.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease and sarcoidosis
 PI asthma, graft versus host disease and diabetes,
 PS Claim 30: Fig 9; 145pp; English.
 CC The present sequence encodes the heavy chain variable region of
 CC murine antibody Act-1. Act-1 is active against human alpha4-beta7
 CC integrin. Muscosal addressin cell adhesion molecule-1 (MacCAM-1) is a
 CC ligand of this particular integrin. The Act-1 antibody interferes with
 CC alpha4-beta7 integrin binding to MacCAM-1, which is present of high
 CC endothelial venules in muscosal lymph nodes. Humanised Act-1 can be used
 CC to inhibit the interaction of cells bearing alpha4-beta7 with cells
 CC bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 SQ Sequence 420 Bp; 104 A; 106 C; 112 G; 98 T;

Query Match 66.5%; Score 359.2; DB 1; Length 420;
 Best Local Similarity 91.0%; Pred. No. 7.1e-85;
 Matches 382; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGAATGACCTGGGCTATCTCTTCTGATCAACAGCTCAAGTGTCCACG 60
 DB 1 ATGGATGAGGCTGATCATCTCTTCTGATCAACAGCTCAAGTGTCCACG 60
 QY 61 GTCCAACTAGTCACTGCTGGGCTGAGTTAGAGCTGGGCTTCAAGTGTCC 120
 DB 61 GTCCAACTAGTCACTGCTGGGCTGAGTTAGAGCTGGGCTTCAAGTGTCC 120
 QY 121 TCGAAGGCTTGGCTACACCTTACACCTGATGATGATGGTGGAGGCGGCT 180
 DB 121 TCGAAGGCTTGGCTACACCTTACACCTGATGATGATGGTGGAGGCGGCT 180
 QY 181 GGCACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 GGCACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 241 CAAAAATTCAGGAGCGCTCATTGATGATGATGATGATGATGATGATGAT 300
 DB 241 CAAAAATTCAGGAGCGCTCATTGATGATGATGATGATGATGATGATGAT 300
 QY 301 GAGCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 301 GAGCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 361 GAGCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 361 GAGCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 420

RESULT 4
 ID 065629
 AC 065629 standard; DNA; 9208 Bp.
 DT 01-FEB-1995 (first entry)
 DE Vector contg. TCAE 8 DNA.
 KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
 OS cell lysis; ss.
 PN MO9411026-A.
 PD 26-MAY-1994.
 PF 12-NOV-1993; U10953.

PR 13-NOV-1992; US-978891.
 PR 03-NOV-1993; US-149099.
 PA (IDEC-) IDEC PHARM CORP.
 PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH,
 PI Refeffe:
 DR WPI: 94-183162/22.
 PT Treating B cell lymphoma with chimeric antibody - against CD20,
 PT causing rapid depletion of peripheral B cells, also new
 PT antibodies and hybridomas
 PS Disclosure: Fig 3; 101pp; English.
 CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric
 CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8
 CC contains 4 transcriptional cassettes, human Ig light and heavy chain
 CC constant regions, dihydrofolate reductase, neomycin phosphotransferase
 CC and murine variable regions. The vector can be used to produce
 CC antibodies which cause depletion of peripheral blood B cells.
 CC including those associated with lymphoma. They mediate complement-
 CC dependent lysis and lyse target cells by antibody-dependent cellular
 CC cytotoxicity.
 CC See also 065629-35.
 SQ Sequence 9208 Bp; 2237 A; 2399 C; 2388 G; 2182 T;

Query Match 65.6%; Score 354.4; DB 1; Length 9208;
 Best Local Similarity 78.5%; Pred. No. 2.7e-83;
 Matches 424; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1 ATGAATGACCTGGGCTATCTCTTCTGATCAACAGCTCAAGTGTCCACG 60
 DB 2400 ATGGATGAGGCTGATCATCTCTTCTGATCAACAGCTCAAGTGTCCACG 2459
 QY 61 GTCCAACTAGTCACTGCTGGGCTGAGTTAGAGCTGGGCTTCAAGTGTCC 120
 DB 2460 GTACAACTAGTCACTGCTGGGCTGAGTTAGAGCTGGGCTTCAAGTGTCC 2519
 QY 121 TCGAAGGCTTGGCTACACCTTACACCTGATGATGATGGTGGAGGCGGCT 180
 DB 2520 TCGAAGGCTTGGCTACACCTTACACCTGATGATGATGGTGGAGGCGGCT 2579
 QY 181 GGCACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 2580 GGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2639
 QY 241 CAAAAATTCAGGAGCGCTCATTGATGATGATGATGATGATGATGATGAT 300
 DB 2640 CAGAGTTAAAGGAGGCGCATGATGATGATGATGATGATGATGATGAT 2699
 QY 301 GAGCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 2700 GAGCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2759
 QY 361 GAGCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 2760 TACGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2819
 QY 421 GGCCTCAGGAGGCGCATGCTTCCCGGAGACCTCTCTCAAGAGCACTTGG 480
 DB 2820 GGTAGCAGGAGGCGCATGCTTCCCGGAGACCTCTCTCAAGAGCACTTGG 2879
 QY 481 GGCACAGCGGCGCTGGGCTGCTGATGATGATGATGATGATGATGATGAT 540
 DB 2880 GGCACAGCGGCGCTGGGCTGCTGATGATGATGATGATGATGATGATGAT 2939

RESULT 5
 ID V20089
 AC V20089 standard; DNA; 428 Bp.
 DT 14-JUL-1998 (first entry)
 DE DNA sequence of murine variable heavy chain region of clone H2B#34.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal addressin cell adhesion molecule-1; MacCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;

KW	leukocyte infiltration of tissue; treatment; inflammatory disease;
KW	inflammatory bowel disease; ss.
OS	Mus sp.
FH	Key
FT	Location/Qualifiers
FT	18. .428
FT	/*tag= a
FT	/note="no stop codon given"
PN	W09806248-A2.
PD	19-FEB-1998.
PF	06-AUG-1997; U13884.
PR	15-AUG-1996; US-700737.
PA	(LEUK-) LEUKOSITE INC.
PI	Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DU, Saldanha JM.
DR	WPT: 98-150172/14.
P-ESDB	W53818.
PT	Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
PT	used for treating inflammatory disease, pancreatitis, diabetes,
PT	asthma, graft versus host disease and sarcoidosis
PS	Example 1: Fig 2: 145pp: English.
CC	The present sequence represents the nucleotide sequence comprising the
CC	variable region of murine Act-1 antibody determined from clone H2B#34.
CC	Act-1 is active against human alpha4-beta1 integrin. Muscosal addressin
CC	cell adhesion molecule-1 (MacDM-1) is a ligand of this particular
CC	integrin. The Act-1 antibody interferes with alpha4-beta7 integrin binding
CC	to MacDM-1, which is present of high endothelial venules in mucosal
CC	lymph nodes. The present sequence was used to construct chimeric,
CC	humanised Act-1 antibodies, which contain murine antigen binding-regions.
CC	The humanised immunoglobulin can be used to inhibit the interaction of
CC	cells bearing alpha4-beta7 with cells bearing a ligand for alpha-beta7.
CC	It can be used for inhibiting leukocyte infiltration of tissues, e.g. for
CC	treating inflammatory diseases such as inflammatory bowel disease. The
CC	immunoglobulin can also be used for detection, isolation and diagnosis.
SO	Sequence 428 Bp: 108 A: 104 C: 115 G: 101 T:

Query Match	64.0%;	Score 345.4;	DB 1;	Length 428;
Best Local Similarity	90.0%;	Pred. No. 2.8e-81;		
Matches 370;	Conservative	0;	Mismatches 41;	Indels 0;
			Gaps	0;

Oy	1	ATGAATACACCTGGGGTATTCCTCTTCTGGATACAGCTACAAAGTGCACCTCCAG	60
Db	18	ATGGGATGGAGCTAATATATCTCTCTTGGATCAACAGCTACAAAGTGCACCTCCAG	77
Oy	61	GTCCACTAGTACGACTGTGGGGCTGAGGTTAAGAACCTGGGGCTTCAGTAAAGGTGCC	120
Db	78	GTCCACTAGTACGACACCTGGGGCTGAGGCTTGGAAAGCTCGGGACTTCAGTAAAGGTGCC	133
Oy	121	TGCAGGGTTCGGGTAAACCTTCACACAGCTACTGGAATGCAATTGGGTATGACGAGCGCT	188
Db	138	TGCAGGGTTCATGGGTAAACCTTCACACAGCTACTGGAATGCACTGGGTATACGAGGCGCT	197
Oy	181	GGCCACAGCTCTAGATGTGATCGGAGAGATGTATCTCTTGGAGATTAATCTAACTACAT	244
Db	198	GGACAGGCGTTAGATGATGATGAGAGATGTATCTCTTGGAGATTAATCTAACTACAT	257
Oy	241	CAAAATTCAAAGGAGCGGCTCACATTGACTGATGACATTCCTCGGTAGCAGACGCTACATG	300
Db	258	CAAAATTCAAAGGAGCGGCGCACCATGACTGATGACATTCCTCGGAGCAGCGCTACATG	317
Oy	301	GAGCTCAGACGCGCTGAGATCTGAGGACACACTGGCGTCTACTATTGTGCAAGAGGGGGTTAC	366
Db	318	CAGCTCAGACGCGCTGACATCTGAGGAGACCTCGCGGCTCTACTATTGTGCAAGAGGGGGTTAC	377
Oy	361	GAGCGATGGGACTATGCATATGACTACTGAGGGGTCAAGGACCGCTGCTACCC	411
Db	378	GAGCGATGGGACTATGCATATGACTACTGAGGGGTCAAGGACCATCAGTACCC	428

RESULT	6
T08482	
ID	T08482 standard; DNA; 750 BP
AC	T08482;

DT	02-APR-1996 (first entry)	
DE	Chimeric heavy chain 5G1.IM1 VL Hg1 DNA.	
KW	Complement C5; haemolysis; kidney; glomerulonephritis;	
KW	monoclonal antibody; antiinflammatory; antibody engineering;	
KW	humanised antibody; complementarity determining region; CDR;	
KW	chimeric antibody; Fab; ds.	
OS	Synthetic.	
FT	key	Location/Qualifiers
FT	cds	1..750
FT		/*tag= a
FT	signal_peptide	1..57
FT		/*tag= b
FT	mat_peptide	58..747
FT		/*tag= c
FN	W09529697-A1.	
PD	09-NOV-1995.	
PF	01-MAY-1995; U05668.	
PR	02-MAY-1994; US-236208.	
PA	(ALEX-) ALEXION PHARM INC.	
PI	Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;	
PI	Rother RP, Springhorn J P, Squinto SP, Thomas TC;	
PI	Wang Y, Wilkins JA;	
DR	WPI: 95-392923/50.	
DR	P-PDB: R776609.	
PT	Treating glomerulonephritis with antibody against complement C5	
FT	component - to inhibit complement induced cell lysis	
PS	Claim 26; Page 116-119; 181pp; English.	
CC	A DNA construct (T08481) codes for chimeric light chain 5G1 VL	
CC	HUK (R77608), which can form the light chain portion of a Fab.	
CC	The chimeric light chain includes CDRs derived from mouse anti-C5	
CC	monoclonal antibody 5G1.1. The DNA can be subcloned with DNA	
CC	(T08482) coding for chimeric Fd (R77609) into vector ALEX-3P (T08476	
CC	for prodn. of chimeric Fab in human 293 EBNA cells. Such recombinan	
CC	antibodies retain the ability of Mab 5G1.1 to block human complement	
CC	C5a generation and thus to reduce glomerular inflammation and kidney	
CC	dysfunction associated with glomerulonephritis.	
CC	Sequence 350 BP; 174 A; 226 C; 191 G; 159 T;	

Query Match	63.28;	Score 341.4;	DB 1;	Length 750;
Best Local Similarity	78.18;	Pred. No. 3.5e-80;		
Matches 424;	Conservative	0;	Mismatches 116;	Indels 3;
			Gaps	1.

Qy	1	ATGAAATGACCTGGGTCATCTCTTTGGTATCAACAGCTACACAAATGTCACCTCCAG	60
Db	1	ATGAAATGACCTGGGTCATCTCTTTGGTATCAACAGCTACACAAATGTCACCTCCAG	60
Qy	61	GTCCAACTAGTGCAGTCTGGGGCTGAGGTTAAGAAGCTGGGGCTTCAGTGAAGTGTCC	120
Db	61	GTTGAGCTGCAGCAGTCTGGAGCTGAGACTGATGAAGCTGGGGCTCAGTGAAGATGTCC	120
Qy	121	TGCAAGGTTCTGGCTACACCTTCACCAAGCTACTGATGCATTGGGTGAGGCAAGCGCCT	180
Db	121	TGCAAGGCTACTGGCTACATTTTCAGTAACACTAGTGATACAGTGGATGAAGCAGAGCGCT	180
Qy	181	GGCCAAAGCTCTAGAGTGGATCGGAGAAATTGATCCTCTCTGAGAGTAATTAATACTACAAT	240
Db	181	GGCAATGGCCTTGGATGGATTTGGTGAATTTTAACTCTGGAAGTGGTTCCTAGTGAATCACT	240
Qy	241	CAAAATTCAGGGAGCGGTACATTGACGTGACATTTCCGCTAGCAGGCTACATG	300
Db	241	GAGAACTTCAAGGACAAAGGCGCATTTCACTGCAAGATATCAATCTTCCAAACAGGCTTAATG	300
Qy	301	GAGCTCAGACACCTGAGATCTGAGAGCACTGCGGTCTACTATTGTGCAGAGGGGGTTAC	360
Db	301	CAACTCAGACACCTGACATCTCAGAGAACTCTGCCGTCTATTACTGTGCAAAATATTCTTTC	360
Qy	361	GACGGATG--GCACTATGCTATTGACTACTAGGGGTCAAGGCAACCTCGTCAACCGTTC	417
Db	361	GGTAGTAGCCCACTGTGACTTGATGTCTGGGGCCGAGGAAACAGGTCAACCGTTC	420
Qy	418	TCAGCTTCACCAAGGGGCCATGGGTCTTCCCTGGACACTCTCCCAAGAGCACTCT	477
Db	418	TCAGCTTCACCAAGGGGCCATGGGTCTTCCCTGGACACTCTCCCAAGAGCACTCT	477

Db 421 TCACCTCCACCAAGGGCCATCGCTCTCCCGCCCTCTCCACAGACCACTCT 480
 QY 478 GGGGCGACAGCGCCCTGGGCTGCTGCTGACAGACTACTTCCCGAAGCGGTGACGTG 537
 Db 481 GGGGCGACAGCGCCCTGGGCTGCTGCTGACAGACTACTTCCCGAAGCGGTGACGTG 540
 QY 538 TCG 540
 Db 541 TCG 543

RESULT 7

T62931
 ID T62931 standard; cDNA; 1389 BP.
 AC T62931;
 DT 16-JUN-1997 (first entry)
 DE 2A2 (Chimeric) human G2/G4 chimeric antibody cDNA.
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis; ss.
 OS Chimeric Homo sapiens;
 OS Chimeric Mus sp.
 PN M09711971-A1.
 PD 03-APR-1997.
 PF 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans M.J., Mattis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR WPI; 97-212855/19.
 DR P-PSDB; W14933.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosures; Page 42-44; 105pp; English.
 CC A cDNA clone (T62931) codes for a chimeric antibody (W14933)
 CC comprising the C1 and hinge regions of human IgG2 and the C2 and C3
 CC regions of human IgG4 (G2/G4 Mab) and a murine anti-porcine soluble
 CC vascular cell adhesion molecule (VCAM) monoclonal antibody (Mab) 2A2
 CC heavy chain variable region sequence (see also T62930). A 2A2
 CC human G2/G4 expression plasmid insert sequence is provided in
 CC T62932. The chimeric antibody is specific for porcine VCAM. It is
 CC useful for diagnosing human rejection of porcine xenotransplants
 CC and for improving xenotransplantation of porcine cells, tissues and
 CC organs into human recipients.
 SQ Sequence 1389 BP; 324 A; 425 C; 371 G; 269 T;

Query Match

Best Local Similarity 78.0%; Score 334.8; DB 1; Length 1389;
 Matches 421; Conservative 0; Mismatches 107; Indels 12; Gaps 1;

QY 1 ATGAATGACCTGGGCTGCTCTTCTTGGTATCAACAGCTACAGTCTCCACG 60
 Db 1 ATGGGATGGAGCTATATCATGTTCTTCTGTATCAACAGCTACAGTCTCCACG 60
 QY 61 GTCCAACTAGTACGCTGGGCTGAGGTTAAGAAGCTGGGGTTAGAGAGTCTCC 120
 Db 61 GTTCACTAGTACGCTGGGCTGAGGTTAAGAAGCTGGGGTTAGAGATATATCC 120
 QY 121 TGCAGAGCTTCTGGCTACACCTTCACCAAGCTAGTATGATGGTGGAGGAGCCCT 180
 Db 121 TGCAGAGCTTCTGGTATCTATTCATTCACCAAGCTATGATGATGGTGGAGGAGCCCT 180
 QY 181 GGCACAGCTAGAGTGGATGGAAGATGATCTCTGAGAGTAATTAATACTAACAAT 240
 Db 181 GGCACAGCTAGAGTGGATGGAAGATGATCTCTGAGAGTAATTAATAATAATTAAT 240
 QY 241 CAATTAATTAAGAGCGGTACATGAGTACATTAATTCGGTAGACAGCCTAATG 300
 Db 241 CAGAGTTAAAGAGCGGTACATTAATGAGTACATTAATTCCTCAACACAGCCTAATG 300

QY 301 GAGCTCAGACAGCTGAGATGTAGAGACACTGCGGTCTACTATTGTGCAAGAGGGGTTAC 360
 Db 301 CAATTCCAGCGCCGATCTTGTAGAGACTGCGGTCTATTACTATCAAGAGGGG----- 356
 QY 361 GAGGATGAGGACATATGATTAATGAGTATGAGGTCACAGGACCCCTGACCCCTCTCA 420
 Db 356 -----AGGTTCTGCTGCTTACTGAGGAGGAGGAGTGTGCTGCTGCA 408
 QY 421 GCCTCCACAGAGGCCATGCTTCTCCCTGGACACCTCTCTCAAGAGACACTCTGGG 480
 Db 409 GCCTCCACAGAGGCCATGCTTCTCCCTGGAGGAGGAGTGTGCTGCTGCA 468
 QY 481 GGCACAGCGCCCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 Db 469 AGACAGCGCCCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528

RESULT 8

T62930
 ID T62930 standard; DNA; 1392 BP.
 AC T62930;
 DT 16-JUN-1997 (first entry)
 DE Murine anti-porcine VCAM 2A2 heavy chain DNA sequence.
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis; ss.
 OS Mus sp.
 PN M09711971-A1.
 PD 03-APR-1997.
 PF 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans M.J., Mattis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR WPI; 97-212855/19.
 DR P-PSDB; W14932.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosures; Page 40-42; 105pp; English.
 CC DNA sequences (T62929-30) respectively code for the light chain
 CC (W14931) and heavy chain (W14932) of murine anti-porcine soluble
 CC vascular cell adhesion molecule (VCAM) monoclonal antibody (Mab)
 CC 2A2. Hybridoma 2A2 was produced by standard techniques using
 CC recombinant, soluble porcine VCAM as immunogen. Chimeric
 CC antibodies can be produced by cloning Mab 2A2 and 3F4 (see also
 CC T62934-35) variable regions into expression plasmid pAPEx-3P
 CC modified to contain the human gamma4 constant region in place of
 CC the human gamma1 C1 region. Sequences are provided for 2A2
 CC (chimeric) human G2/G4 cDNA (T62931), a 2A2 human G2/G4 expression
 CC plasmid insert (T62932), and a 2A2 human IgG4 expression plasmid
 CC insert (T62933). The chimeric antibodies are specific for porcine
 CC VCAM. They are useful for diagnosing human rejection of porcine
 CC xenotransplants and for improving xenotransplantation of porcine
 CC cells, tissues and organs into human recipients.
 SQ Sequence 1392 BP; 326 A; 421 C; 373 G; 272 T;

Query Match

Best Local Similarity 62.0%; Score 334.8; DB 1; Length 1392;
 Matches 421; Conservative 0; Mismatches 107; Indels 12; Gaps 1;

QY 1 ATGAATGACCTGGGCTGCTCTTCTTGGTATCAACAGCTACAGTCTCCACG 60
 Db 1 ATGGGATGGAGCTATATCATGTTCTTCTGTATCAACAGCTACAGTCTCCACG 60
 QY 61 GTCCAACTAGTACGCTGGGCTGAGGTTAAGAAGCTGGGGTTAGAGAGTCTCC 120
 Db 61 GTTCACTAGTACGCTGGGCTGAGGTTAAGAAGCTGGGGTTAGAGATATATCC 120
 QY 121 TGCAGAGCTTCTGGCTACACCTTCACCAAGCTAGTATGATGGTGGAGGAGCCCT 180
 Db 121 TGCAGAGCTTCTGGCTACACCTTCACCAAGCTAGTATGATGGTGGAGGAGCCCT 180


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FT      Intron      2447. .2564
FT      exon        /+tag- f
FT      exon        2565. .2894
FT      Intron      /+tag- g
FT      Intron      2985. .2991
FT      exon        /+tag- h
FT      exon        2992. .3314
FT      Intron      /+tag- i
FT      Intron      3315. .4045
FT      exon        /+tag- j
FT      exon        4046. .4198
FT      Intron      /+tag- k
FT      Intron      4199. .4428
FT      exon        /+tag- l
FT      exon        4429. .5177
FT      exon        /+tag- m
FT      exon        /codon_start- 4461

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PN      MO9711971-A1.
PD      03-APR-1997.
PE      27-SEP-1996; US-004489.
PR      28-SEP-1995; US-004489.
PR      26-SEP-1996; US-004489.
PA      (ALEX-) ALEXION PHARM INC.
PI      Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
PI      Rother RP;
PI      WPI; 97-212855/19.
DR      P-PSDB; W14935;
DR      P-PSDB; W14936.
PT      Antibodies binding to porcine but not human cell interaction
PT      proteins - useful to treat and assay for rejection of xenografted
PT      porcine organs, tissues or cells
PS      Disclosure; Page 47-52; 105pp; English.
CC      A DNA sequence (T62933) comprises a 2A2 human IgG4 expression
CC      plasmid insert sequence. It is obid. by cloning the light chain
CC      (see also T62929) and heavy chain (see also T62930) variable
CC      region sequences of murine anti-porcine vascular cell adhesion
CC      molecule (VCAM) monoclonal antibody 2A2 into an expression plasmid
CC      modified to contain the human gamma4 constant region in place of
CC      the human gamma C1 region. The encoded heavy chain (W14935) and
CC      light chain (W14936) can be used to produce a chimeric antibody
CC      that is specific for porcine VCAM. The chimeric antibody is useful
CC      for diagnosing human rejection of porcine xenotransplants and for
CC      improving xenotransplantation of porcine cells, tissues and organs
CC      into human recipients.
SQ      Sequence 5250 BP; 1236 A; 1469 C; 1352 G; 1193 T;

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Query Match      62.08; Score 334.8; DB 1; Length 5250;
Best Local Similarity 78.08; Pred. No. 2.9e-78;
Matches 421; Conservative 0; Mismatches 107; Indels 12; Gaps 1;

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QY      1 ATGAATGACACCTGGGATCTCTCTTGTATCAACAGCTAAGTCCATCCAG 60
DB      1318 ATGGGATGGAGATATATCTTCTTGTATCAACAGCTAAGTCCATCCAG 1377
QY      61 GTCCAACTAGTCACTGGGCTGAGGTTAAGAAGCTGGGGCTCAGTGAAGTTC 120
DB      1378 GTCAACTGACAGCATCTGGGCTCAGCTGTTAGGCTGGGATTCAGTAATATCC 1437
QY      121 TGCAGGGTCTGGCTACACCTTCACAGCTACTGATGATGGTGGAGGAGCCCT 180
DB      1438 TGCAGGCTCTGGTACTCTATTCACAGCTATGATGATGATGATGATGATGAT 1497
QY      181 GGCACAGCTGAGTGGATGAGGATGATGATGATGATGATGATGATGATGATGAT 240
DB      1498 GGCACAGCTGAGTGGATGAGGATGATGATGATGATGATGATGATGATGATGAT 1557
QY      241 CAAATATCAAGGACGACCATTCATGATGATGATGATGATGATGATGATGATGATGAT 300
DB      1558 CAGAGGTTAAAGGACGACCATTCATGATGATGATGATGATGATGATGATGATGATGAT 1617
QY      301 GAGCTGACAGCCTGAGATCTGAGGACATGCGGCTTACTATTTGTGCAAGGGGGTTAC 360

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DB      1618 CAATTCAGCGGCCGACTCTGAGGACTGCGGCTTATTACTGTACAAAGAGGG- 1673
QY      361 GAGGATGGGACTATGCTATGACTGAGGATCAAGGACACCTGGTCACTGCTCTCA 420
DB      1673 -----AGCTTTCGTCGTTGCTTACTGAGGACGAGGAGGACTGTGCTCTGCA 1725
QY      421 GCCTCCACCAAGGAGCCCATGCTTCTCCCTGGACACCTCTCTCCCAAGACACCTG 480
DB      1726 GCCTCCACCAAGGAGCCCATGCTTCTCCCTGGACACCTCTCTCCCAAGACACCTG 1785
QY      481 GGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCAAGCCGAGGAGTCTG 540
DB      1786 AGCAGACGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCAAGCCGAGGAGTCTG 1845

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RESULT 11

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ID      T62935
AC      T62935 standard; DNA; 1395 BP.
DT      16-JUN-1997 (first entry)
DE      Murine anti-porcine VCAM 3F4 heavy chain DNA sequence.
KM      Xenotransplantation; graft rejection; cell interaction; pig;
KM      vascular cell adhesion molecule; VCAM; monoclonal antibody;
KM      chimeric antibody; diagnosis; ss.
OS      Mus sp.
PN      MO9711971-A1.
PD      03-APR-1997.
PE      27-SEP-1996; US-004489.
PR      28-SEP-1995; US-004489.
PR      26-SEP-1996; US-004489.
PA      (ALEX-) ALEXION PHARM INC.
PI      Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
PI      Rother RP;
PI      WPI; 97-212855/19.
DR      P-PSDB; W14938.
PT      Antibodies binding to porcine but not human cell interaction
PT      proteins - useful to treat and assay for rejection of xenografted
PT      porcine organs, tissues or cells
PS      Disclosure; Page 53-55; 105pp; English.
CC      DNA sequences (T62934-35) respectively code for the light chain
CC      (W14937) and heavy chain (W14938) of murine anti-porcine soluble
CC      vascular cell adhesion molecule (VCAM) monoclonal antibody (Mab)
CC      3F4. Hybridoma 3F4 was produced by standard techniques using
CC      recombinant, soluble porcine VCAM as immunogen. Chimeric
CC      antibodies can be produced by cloning Mab 3F4 and 2A2 (see also
CC      T62929-30) variable regions into expression plasmid pAPEX-3P
CC      modified to contain the human gamma4 constant region in place of
CC      the human gamma C1 region. Sequences are provided for 3F4
CC      (chimeric) human G2/G4 cDNA (T62936), a 3F4 human G2/G4 expression
CC      plasmid insert (T62937), and a 3F4 human IgG4 expression plasmid
CC      insert (T62938). The chimeric antibodies are specific for porcine
CC      VCAM. They are useful for diagnosing human rejection of porcine
CC      xenotransplants and for improving xenotransplantation of porcine
CC      cells, tissues and organs into human recipients.
SQ      Sequence 1395 BP; 322 A; 429 C; 379 G; 265 T;

```

```

Query Match      61.98; Score 334.4; DB 1; Length 1395;
Best Local Similarity 77.88; Pred. No. 2.7e-78;
Matches 420; Conservative 0; Mismatches 111; Indels 9; Gaps 1;

```

```

QY      1 ATGAATGACACCTGGGATCTCTCTTGTATCAACAGCTAAGTCCATCCAG 60
DB      1 ATGAATGACAGCTGGGATTTCTTCTCTGCTCACTAAGTCCAGTCCAG 60
QY      61 GTCCAACTAGTCACTGGGCTGAGGTTAAGAAGCTGGGGCTCAGTGAAGTTC 120
DB      61 GTTCAGTTCACAGAGCTGTGGGGCTGAGCTGCAAGACCTTGGCTTCAGTAAGTTC 120
QY      121 TGCAGGGTCTGGCTACACCTTCACAGCTACTGATGATGGTGGAGGAGGCGCT 180
DB      121 TGCAGGCTCTGGCTACAAATTTAATGATGATGATGATGATGATGATGATGATGATGAT 180

```


PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure; Page 58-61; 105pp; English.
 CC A DNA sequence (T62937) comprises a 3p4 human G2/G4 (see also
 CC T62936) chimeric antibody expression plasmid insert sequence.
 CC The chimeric antibody (W14940) is specific for porcine vascular
 CC cell adhesion molecule (VCAM) and is useful for diagnosing human
 CC rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into
 CC human recipients.
 SQ Sequence 3400 BP; 759 A; 1012 C; 909 G; 720 T;

Query Match 61.9%; Score 334.4; DB 1; Length 3400;
 Best Local Similarity 77.8%; Pred. No. 3.3e-78;
 Matches 420; Conservative 0; Mismatches 111; Indels 9; Gaps 1;

QY 1 ATGAATGACCTGGGCTCTCTCTTGTATCAACAGCTACAGTCCACTCCAG 60
 DB 1350 ATGAATGACCTGGGCTCTCTCTTGTATCAACAGCTACAGTCCACTCCAG 1409
 QY 61 GTCCAACTAGTACGAGTCTGGGGCTGAGTTAGAACCTGGGGCTGAGTGGTCC 120
 DB 1410 GTTCAGCTCCAGAGCTCTGGGGCTGAGTTAGAACCTGGGGCTGAGTGGTCC 1469
 QY 121 TGCAGAGGCTCTGGCTACACCTTACAGCTAGTATGATGGTGGAGGAGGCGCT 180
 DB 1470 TGCAGAGGCTCTGGCTACATTTTAAATGATGATGATGAGTGGTGGTAAACAGAGGCT 1529
 QY 181 GGCACAGCTCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 1530 GGCACAGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1589
 QY 241 CAAAATTCAGAGGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 1590 CAAAATTCAGAGGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1649
 QY 301 GAGCTCAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 1650 CAACTCAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1709
 QY 361 GACGATGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 1710 GAGAGCT-----ACTTTGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1760
 QY 421 GCTTCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
 DB 1761 GCTTCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1820
 QY 481 GGCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 DB 1821 AGCACAAGCGCGCTGGGCTCTGCTGATGATGATGATGATGATGATGATGATGAT 1880

RESULT 14

T62938
 ID T62938 standard; DNA; 5300 BP.
 AC T62938:
 DT 16-JUN-1997 (first entry)
 DE 3p4 human 19g4 expression plasmid insert sequence.
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis; ss.
 OS Chimeric Homo sapiens;
 FH Chimeric Mus sp.
 FH Key Location/Qualifiers
 FT exon 903..1055
 FT /tag- a
 FT 1056..1285
 FT /tag- b
 FT 1286..2055
 FT /tag- c
 FT /codon_start= 1350

FT Intron 2056..2445
 FT /tag- d
 FT 2446..2481
 FT /tag- e
 FT 2482..2599
 FT /tag- f
 FT 2600..2929
 FT /tag- g
 FT 2930..3025
 FT /tag- h
 FT 3026..3349
 FT /tag- i
 FT 3350..4080
 FT /tag- j
 FT 4081..4233
 FT /tag- k
 FT 4234..4463
 FT /tag- l
 FT 4464..5212
 FT /tag- m
 FT /codon_start= 4496

PN MO9711971-1.
 PD 03-APR-1997.
 PE 27-SEP-1996; 015575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rothen RP;
 DR WPI; 97-212855/19.
 DR P-PDB; W14941.
 DR P-PDB; W14942.

PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure; Page 61-67; 105pp; English.
 CC A DNA sequence (T62938) comprises a 3p4 human 19g4 expression
 CC plasmid insert sequence. It is obt. by cloning the light chain
 CC (see also T62934) and heavy chain (see also T62935) variable
 CC region sequences of murine anti-porcine vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 3p4 into an expression plasmid
 CC modified to contain the human gamma4 constant region in plasmid of
 CC the human gamma CI region. The encoded heavy chain (W14941) and
 CC light chain (W14942) can be used to produce a chimeric antibody
 CC that is specific for porcine VCAM. The chimeric antibody is useful
 CC for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs
 CC into human recipients.
 SQ Sequence 5300 BP; 1236 A; 1494 C; 1375 G; 1195 T;

Query Match 61.9%; Score 334.4; DB 1; Length 5300;
 Best Local Similarity 77.8%; Pred. No. 3.7e-78;
 Matches 420; Conservative 0; Mismatches 111; Indels 9; Gaps 1;

QY 1 ATGAATGACCTGGGCTCTCTCTTGTATCAACAGCTACAGTCCACTCCAG 60
 DB 1350 ATGAATGACCTGGGCTCTCTCTTGTATCAACAGCTACAGTCCACTCCAG 1409
 QY 61 GTCCAACTAGTACGAGTCTGGGGCTGAGTTAGAACCTGGGGCTGAGTGGTCC 120
 DB 1410 GTTCAGCTCCAGAGCTCTGGGGCTGAGTTAGAACCTGGGGCTGAGTGGTCC 1469
 QY 121 TGCAGAGGCTCTGGCTACACCTTACAGCTAGTATGATGGTGGAGGAGGCGCT 180
 DB 1470 TGCAGAGGCTCTGGCTACATTTTAAATGATGATGATGATGATGATGATGAT 1529
 QY 181 GGCACAGCTCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 1530 GGCACAGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1589
 QY 241 CAAAATTCAGAGGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 300

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Db 1590 CAGAGTTGAGGGGAGCCAGCATTTGACTGAGATAATCTCCAGCAGACCTTACATG 1649
QY 301 GAGCTCAGACCTGAGATCTGAGAGACATGGGCTCTACTATTGCAAGAGGGGGTAC 360
Db 1650 CACTCAGACCTTGGATCTGAGAGACTCTGGGCTTCTTACTGTGCAAGACCTACGTA 1709
QY 361 GACGATGGAGCTATGCTATTGACTACTGAGGCTCAAGGACACCTGTACCGTCTCTCA 420
Db 1710 GGAGGCT-----ACTTTGACTACTGGGGCCAAAGCAGACACTCTCACAGTCTCTCA 1760
QY 421 GCCTCCACCAAGGGCCCATCGGCTCTCCCTGGACACCTCTCTCAAGACCTCTGG 480
Db 1761 GCTTCACCAAGGGCCCATCGGCTCTCCCTGGGCGCTCTCAAGAGACCTCTCGAG 1820
QY 481 GGCACAGGGCCCTGGGCTGGCTGCTCAAGGACTACTTCCCGAAGCGGTGAGGGTTCG 540
Db 1821 AGCACAGCGCCCTGGGCTGGCTGCTCAAGGACTACTTCCCGAAGCGGTGAGGGTTCG 1880
```

RESULT 15

```
043844
ID 043844 standard; DNA; 11529 BP.
AC 043844; 1993 (first entry)
DE Plasmid pAH4602.
KW Polymerase chain reaction; primer; PCR; amplify; murine;
KW heavy; light; chain; variable; constant; region; anti-human;
KW transferrin; receptor; antibody; brain; capillary;
KW endothelial cell; conjugate; neuropharmaceutical;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy;
KW Parkinsons disease; Alzheimers disease; ss.
OS Synthetic.
FH Key location/Qualifiers
FT unsure 2070..3769
FT cds /*tag- a
FT 3907..4611
FT signal_peptide /*tag- b
FT 3097..3963
FT /*tag- c
FT mat_peptide /*tag- "leader sequence"
FT 3964..4611
FT /*tag- d
FT /*note- "Mature VH/CH region"
FT cds 5000..5044
FT /*tag- e
FT /*note- "Undefined ORF"
FT cds 5163..5492
FT /*tag- f
FT /*note- "Undefined ORF2"
FT cds 5589..5909
FT /*tag- g
FT /*note- "Undefined ORF2"
FT unsure 6118..7321
FT /*tag- h
FT unsure 8177..8201
FT /*tag- i
PN WC9310819-A.
PD 10-JUN-1993.
PE 24-NOV-1992; U10206.
PR 26-NOV-1991; US-800458.
PA (ALKE-) ALKERMES INC.
PI Fiden.PM.
DR WPI: 93-196742/24.
P-PSDB: R41682-85.
PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PS disorders
PS Disclosure: Fig 11A-G; 151PP; English.
CC This sequence represents the expression vector pAH4602.
CC chain variable region (VH) of the antibody 128.1, an
CC ampicillin resistance gene and a histidine (histidinol)
```

```
CC selection marker. Transcription of the VH gene is from the
CC VH promoter of the murine 27.44 gene. The vector also
CC includes a heavy chain immunoglobulin enhancer and the human
CC gamma constant region (CH). The VH region of 128.1 was
CC isolated by polymerase chain reaction and cloned into
CC plasmid pAH4274. This was achieved by digesting the plasmid
CC and the product with EcoRV and NheI. The VH gene was
CC inserted in-frame with the human gamma CH region CH at the
CC 3' end of the VH-J region by means of a NheI site. 128.1 is
CC an anti-human transferrin receptor antibody which binds to
CC the transferrin receptor on brain capillary endothelial
CC cells. This antibody may be used in a conjugate in which it
CC is linked to a neuropharmaceutical or diagnostic agent. The
CC conjugate may be used to treat or prevent neurological
CC disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC Parkinsons and Alzheimers disease. It may also be used for
CC diagnostic methods.
SQ Sequence 11529 BP; 2175 A; 2217 C; 2148 G; 2058 T;
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Query Match 61.6%; Score 332.8; DB 1; Length 11529;
Best Local Similarity 77.6%; Pred. No. 1.2e-77;
Matches 419; Conservative 0; Mismatches 112; Indels 9; Gaps 1;

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QY 1 ATGAATGCACTGGGCTCATCTCTTCTGTGTATCAACAGCTACAGTCCACG 60
Db 3907 ATGAATGAGAGCTGGTAATCTCTCTCTCTCTGTCAGAGAGTGCCTGAG 3966
QY 61 GTCCAACTAGTGCAGTGTGGGCTGAGGTTAAGAAGCTGGGCTTGAAGAGTCC 120
Db 3967 GTCCAGCTGCAACAGTGTGACCTGCAAGCTGTGAGAGCTTGAAGTAATTC 4026
QY 121 TGCAAGGTTCTGGCTACCTTACCTCACCAGCTACTGATGATGCTGGTGAAGGCGCT 180
Db 4027 TGCAAGGCTTGTGTTACTTACTTACTGCTACACCTGAAGTGGTGAAGAGCAT 4086
QY 181 GGCCAGCTCTAGAGTGGATGAGAGATGATGATCTCTGAGAGTAATTAATACTAAT 240
Db 4087 GGAGAGAACTTGTAGTGTGATGAGAGTATTAATCTCACAATGTGTGACTGACTCAAC 4146
QY 241 CAAATTTCAAGGAGCGGCTACATGTGATCTATGATCTTCCGTATGCAAGAGGCTATG 300
Db 4147 CAGAGTTCAAGGAGCAAGGCGCTTAACTGATCAAGATCAACAGAGCGCTATATG 4206
QY 301 GAGCTCAGACCTGAGATCTGAGAGACATGCGGTACTATGTCGAAGAGGGGTTAC 360
Db 4207 GAGTCTCTCACTGATCATCTGAGAGACTCTGCACTTATTAATCTGCAAGAGG----- 4260
QY 361 GACGATGGAGCTATGCTATTGACTACTGGGCTCAAGGACCTGTACCGTCTCTCA 420
Db 4260 --CTACTATTACTATTCTTTGACTACTGGGCTCAAGGACCTGACCGTCTCTCA 4317
QY 421 GCCTCCACCAAGGGCCCATCGGCTCTCCCTGGACACCTCTCTCAAGAGAGACTCTGGG 480
Db 4318 GCTAGCAGCAAGGGCCCATCGGCTCTCCCTGGACACCTCTCTCAAGAGAGACTCTGGG 4377
QY 481 GGCACAGGGCCCTGGGCTGGCTGCTCAAGGACTACTTCCCGAAGCGGTGAGGGTTCG 540
Db 4378 GGCACAGCGCCCTGGGCTGGCTGCTCAAGGACTACTTCCCGAAGCGGTGAGGGTTCG 4437
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Search completed: May 11, 1999, 12:03:35
Job time: 1542 sec

1 MKCIWILFVLSIAISVHSQVQLVQSGAEVKKPGASVKVSCKGSGYTFITSYMMHWVROAL

QY 121 DGMVADPWGGLTVVSS 140
 DB 118 --WRDAFDWGGTMTVSS 135

RESULT 14

PL0011
 Ig heavy chain precursor V region (4C11) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Oct-1996

C:Accession: PL0011

R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.

MOL. Immunol. 25, 33-40, 1988

A:Title: Structural basis of stimulatory anti-idiotypic antibodies.

A:Reference number: PL0011; MUID:88142863

A:Accession: PL0011

A:Molecule type: mRNA

A:Residues: 1-151 <CHP>

A:Experimental source: cell line 4C11

C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>

F:50-54/Region: complementarity-determining 1

F:69-85/Region: complementarity-determining 2

F:118-125/Region: complementarity-determining 3

F:137-151/Domain: C region (fragment) #status predicted <COR>

Query Match 53.0%; Score 506; DB 2; Length 151;
 Best Local Similarity 64.3%; Pred. No. 5.7e-35;

Matches 99; Conservative 18; Mismatches 31; Indels 6; Gaps 2;

QY 1 MKCTVILFLVSTATSVHSGVQLVDSGAEVKKPKGASVYKSCGSGYTFTSYMMHWYRQAP 60

DB 1 MGSWIFLFLSLGAGVLSVQLQDSGPELKPASVYKISCRASGTYFTDTYTMHWKQSH 60

QY 61 GQRLWIEIDPESNTNINQKFKGRVTLVDISASTAYMELSLRSEDTAVYYCARGGY 120

DB 61 GKSLEWIGFPDPNYNTFYNEFKKATLTYDKSSTAYMELSLRSEDSAVYYCA---- 117

QY 121 DGMVADPWGGLTVVSSASTKGPSVPLAP 153

DB 117 -SYDYGALDYWGQGTSTVYSSAKTTPSPVPLAP 149

RESULT 15

MHMS18

Ig heavy chain precursor V region (B1-8) - mouse

N:Contains: Ig heavy chain precursor V region 186-2

C:Species: Mus musculus (house mouse)

C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 20-Mar-1998

C:Accession: A90809; B90809; A22769; A02036

R:Botnwell, A.L.M.; Paskind, M.; Reith, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.

Cell 24, 625-637, 1981

A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: some

A:Reference number: A90809; MUID:81234548

A:Accession: A90809

A:Molecule type: DNA

A:Residues: 1-139 <B18>

A:Cross-references: GB:J00529; NID:g195114; PID:g195115

A:Accession: B90809

A:Molecule type: DNA

A:Residues: 1-117 <1862>

A:Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hap

R:Didrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.

EMBO J. 1, 635-640, 1982

A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between

A:Reference number: A90971; MUID:84236026

A:Accession: A22769

A:Molecule type: protein
 A:Residues: 20-139 <DIL>
 A:Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch V of the mu chain

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-139/Product: Ig kappa chain V region (B1-8) #status experimental <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:118-124/Region: D segment

F:125-139/Region: J segment (JH2)

Query Match 53.0%; Score 505.5; DB 1; Length 139;
 Best Local Similarity 70.4%; Pred. No. 5.7e-35;

Matches 95; Conservative 14; Mismatches 25; Indels 1; Gaps 1;

QY 6 VILFLVSTATSVHSGVQLVDSGAEVKKPKGASVYKSCGSGYTFTSYMMHWYRQAPGRLE 65

DB 6 IMLFLAATATGVHSGVQLQDPGAEIVKPKGASVYKLSCKASGTYFTSYMMHWYKQRRGLE 65

QY 66 WIGELDPESNTNINQKFKGRVTLVDISASTAYMELSLRSEDTAVYYCARGGYDGMV 125

DB 66 WIGRIDPNSGGLTKYNEKFKKATLTYDKPSSSTAYMQLSLRSEDSAVYYCARYDYGGSS 125

QY 126 AIDWGGGLTVVSS 140

DB 126 -FDWGGGLTVVSS 139

Search completed: May 11, 1999, 12:23:24
 Job time: 297 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 1999, 12:20:08 ; Search time 22.45 Seconds

(without alignments)
215,201 Million cell updates/sec

Title: US-08-700-737-19

Perfect score: 954
Sequence: 1 MACTWVILFLVSTAFVSHSQ.....GTAALGLVKKYFPEPTVS 180

Scoring table: BLOSUM62

Searched: 74019 seqs, 26840295 residues

Database: SwissProt_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	505.5	53.0	139	1	HV07_MOUSE
2	491	51.5	138	1	HV48_MOUSE
3	471	49.4	117	1	HV16_HUMAN
4	470	49.3	117	1	HV06_MOUSE
5	467	49.0	140	1	HV02_MOUSE
6	465.5	48.8	137	1	HV11_MOUSE
7	455	47.7	117	1	HV18_MOUSE
8	453.5	47.5	143	1	HV1C_HUMAN
9	447	46.9	117	1	HV05_MOUSE
10	445	46.6	117	1	HV09_MOUSE
11	443	46.4	117	1	HV04_MOUSE
12	443	46.4	136	1	HV15_MOUSE
13	437.5	45.9	120	1	HV30_MOUSE
14	433	45.4	117	1	HV49_MOUSE
15	427	44.8	117	1	HV03_MOUSE
16	425	44.5	120	1	HV03_MOUSE
17	421.5	44.2	118	1	HV51_MOUSE
18	419	43.9	117	1	HV12_MOUSE
19	417	43.7	117	1	HV13_MOUSE
20	414	43.4	117	1	HV14_MOUSE
21	398	41.7	117	1	HV52_MOUSE
22	394	41.3	121	1	HV01_MOUSE
23	366	38.4	117	1	HV01_MOUSE
24	363.5	38.1	114	1	HV00_MOUSE
25	354	37.1	125	1	HV1E_HUMAN
26	352.5	36.9	136	1	HV16_MOUSE
27	352	36.9	142	1	HV01_RAT
28	351.5	36.8	124	1	HV1D_HUMAN
29	350	36.7	117	1	HV42_MOUSE
30	347.5	36.4	119	1	HV37_MOUSE
31	347.5	36.4	119	1	HV38_MOUSE
32	347	36.4	121	1	HV3J_HUMAN
33	346.5	36.3	120	1	HV1H_HUMAN
34	341	35.7	117	1	HV41_MOUSE
35	339.5	35.6	119	1	HV40_MOUSE
36	334.5	35.1	122	1	HV3G_HUMAN
37	333	34.9	118	1	HV39_MOUSE
38	330.5	34.6	122	1	HV3H_HUMAN
39	327.5	34.3	124	1	HV1E_HUMAN
40	327	34.3	123	1	HV25_MOUSE
41	325.5	34.1	126	1	HV3K_HUMAN
42	319	33.4	115	1	HV3D_HUMAN
43	318.5	33.4	116	1	HV3T_HUMAN

ALIGNMENTS

44 318 33.3 115 1 HV32_MOUSE P01801 mus musculu
45 317.5 33.3 122 1 HV3A_HUMAN P01762 homo sapien

```

RESULT 1
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751: P01752:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE: 81234548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
  BALTIMORE D.;
  CELL 24:625-637(1981).
RL -1- THE B1-8 MO CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
  ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
  ANTIBODIES).
DR EMBL: J00529; GI95115; -.
DR PIR: A02034; MEMS18.
DR HSSP: P01810; 1JHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION (B1-8 / 186-2).
FT CHAIN 20 139 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139
SQ SEQUENCE 139 AA; 15419 MW; DEB2C7DA CRC32;

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Query Match 53.0%; Score 505.5; DB 1; Length 139;
Best Local Similarity 70.4%; Pred. No. 1.1e-40;
Matches 95; Conservative 14; Mismatches 25; Indels 1; Gaps 1;

```

QY 6 VILFIVSTATSVHSONVQVLOGSAEYKRGASVYVSCSGGYFTSYWMHVRQAPQORLE 65
  ::::: ||| ||||| |||: |||||: ||| |||||: ||: ||
DB 6 IMFLPSTATGVHSONVQVLOGPAGALVPGASVYLSCASGYFTSYWMHVRQAPQORLE 65
QY 66 WIGEIDPESSENTNYNOKFGKRVTLVDISASTAYMELSLSRSDTAAYVYCARGYDGMWD 125
  ||| |||: | ||||: ||||| |||||: ||| |||||: ||| |||
DB 66 WIGRIDPNSGCTGYNEFKKATLTVDKPSTAYMQLSLTSDSAVYVYCARDYGSY 125
QY 126 AIDYWGQGLVTVSS 140
  ||||| ||||| |||||
DB 126 -FDYWGQGLTVTVSS 139

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RESULT 2
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980:
DT 23-OCT-1986 (REL. 02, CREATED)
DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (TEPC 1017).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 84248078.
 RA GILLIAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F.,
 RA TUCKER P.W.,
 RL PROC. NATL. ACAD. SCI. U.S.A. 81:4164-4168(1984).
 DR HSP: A02033; HVMST7.
 DR HSP: P01810; 1JHL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 138 IG HEAVY CHAIN V REGION (TEPC 1017).
 FT DOMAIN 21 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 128 138 FRAMEWORK 4.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 138 138
 SQ SEQUENCE 138 AA; 15576 MW; BEF6247B CRC32;

Query Match 51.5%; Score 491; DB 1; Length 138;
 Best Local Similarity 66.0%; Pred. No. 2,4e-39;
 Matches 93; Conservative 21; Mismatches 23; Indels 4; Gaps 2;

QY 1 MKCTWILFLVSTATSVHSOVOLVOSGAEVKKPGASVYVCKSGGYTFTSYMHVWVQAP 60
 DB 1 MGWSYILFLVATADVHSOVOLVOPGAEVKKPGASVYVCKSGGYTFTSYMHVWVQAP 60
 QY 61 GORLEWIGELIDPSESNYNOKEFGKRVLTVDISASTAYMELSLRSDTAIVYCCAR-G 119
 DB 61 GGGLEWIGELIDPSESNYNOKEFGKRVLTVDISASTAYMELSLRSDTAIVYCCAR-G 120
 QY 120 YDGDVDAIDWGGGTLYTSS 140
 DB 121 YYDW---FVYWGQGLTVTFSA 138

RESULT 3
 HVLG_HUMAN STANDARD; PRT; 117 AA.
 AC P23083;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 DE 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V-I REGION (V35).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88296408.
 RA MATSUDA F., LEE K.R., NAKAI S., SATO T., KODAIRA M., ZONG S.Q.,
 RA OHNO H., FUKUHARA S., HONJO T.,
 RL EMBO J. 7:1047-1051(1988).
 DR EMBL; X07448; -. NOT_ANNOTATED_CDS.
 DR PIR; S00476; HVMU35.
 DR HSP: P01810; 1JVB.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (V35).
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13009 MW; FFA560D1 CRC32;

Query Match 49.4%; Score 471; DB 1; Length 117;
 Best Local Similarity 76.9%; Pred. No. 1,5e-37;
 Matches 90; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

DB 1 MDWTRILFLVAAATGASHOVOLVOSGAEVKKPGASVYVCKSGGYTFTSYMHVWVQAP 60
 QY 61 GORLEWIGELIDPSESNYNOKEFGKRVLTVDISASTAYMELSLRSDTAIVYCCAR 117
 DB 61 GGGLEWIGELIDPSESNYNOKEFGKRVLTVDISASTAYMELSLRSDTAIVYCCAR 117

RESULT 4
 HVO6_MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (102).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-C57BL/6;
 RX MEDLINE; 81234548.
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,
 RA BALTIMORE D.,
 RL CELL. 24:625-637(1981).
 CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 CC THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 DR HSP: A02032; HVMST2.
 DR HSP: P01810; 1JHL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (102).
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 41 115 FRAMEWORK 3.
 FT NON_TER 117 117 BY SIMILARITY.
 SQ SEQUENCE 117 AA; 12867 MW; 4BDD1982 CRC32;

Query Match 49.3%; Score 470; DB 1; Length 117;
 Best Local Similarity 79.3%; Pred. No. 1,8e-37;
 Matches 88; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 6 VILFLVSTATSVHSOVOLVOSGAEVKKPGASVYVCKSGGYTFTSYMHVWVQAPGORE 65
 DB 6 IILFLVATGAVSHVSHVLOOPGAEVKKPGASVYVCKSGGYTFTSYMHVWVQAPGORE 65
 QY 66 WIGLIDPSESNYNOKEFGKRVLTVDISASTAYMELSLRSDTAIVYCCAR 116
 DB 66 WIGLIDPSESNYNOKEFGKRVLTVDISASTAYMELSLRSDTAIVYCCAR 116

RESULT 5
 HVO2_MOUSE STANDARD; PRT; 140 AA.
 AC P01746;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (9367).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-A/J;
 RX MEDLINE; 82152818.
 RA STMS J., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
 RA CAPRA J.D.;

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Oy      6 VILELVSTATSYHSQVOVLQSGAEVKKPGASVVKVSCGSGYTFTSYMMHWVRQAPQRL 65
        ::||: ||| ||||| | | | |||||: || | ||||| |||| | ||: ||
Db      6 IMLFLAATATGVSQVOVLQPGAEVKKPGASVKKLSCKSKSGYFTFTSYLMHWVRQPRGLE 65

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RP SEQUENCE OF 16-142.
RA BERNICK H.H., JOHANSSON S.G.O., VON BAHR-LINDSTROM H.,
RL (IN) IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS
RL BACH M.K., ED., PP.1-36. MARCEL DEKKER, NEW YORK, (1978).
RC -1- THIS EPSILON CHAIN WAS ISOLATED FROM A MIELOMA PROTEIN.
CR PIR; A02026; EIHOND.

DR HSSP; P01607; 1REV.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT NON CONS 4 5
 FT SIGNAL 1 15
 FT CHAIN 16 143 IG HEAVY CHAIN V REGION (ND).
 FT MOD_RES 16 16 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 37 111
 FT CONFLICT 17 17 T -> V (IN REF. 2).
 FT CONFLICT 49 50 IH -> HI (IN REF. 2).
 FT CONFLICT 63 64 VG -> GV (IN REF. 2).
 FT CONFLICT 121 121 MISSING (IN REF. 2).
 FT NON_TER 143 143
 SQ SEQUENCE 143 AA; 16051 MW; 6D605E13 CRC32;

Query Match 47.5% Score 453.5; DB 1; Length 143;
 Best Local Similarity 62.6% Pred. No. 8.1e-36;
 Matches 87; Conservative 20; Mismatches 25; Indels 7; Gaps 2;

QY 9 FLVSTATSVHSQVOLVSGAEVKKPGASVSKSGSGYTFSTYMHVWVROAPGQRLWIG 68
 DB 5 FLVAAATFVHSQTLVSGAEVKKPGASVSKSGSGYTFSTYMHVWVROAPGQRLWIG 64
 QY 69 EIDSESTNTNOKFKGVTLTVDISASTAMELSLSRSEDTAVYYCAR-----GGYDGM 123
 DB 65 WINPNSGGTNTAPRFGQVTVTRDASFSTAYMDLSRLSDSAVAYCAKSPFMSDYNE 124
 QY 124 DYA--IDYWGGLTVTVSS 140
 DB 125 DYSTLDWVGQTVTVSS 143

RESULT 9
 HV05_MOUSE STANDARD; PRT; 117 AA.
 ID HV05_MOUSE
 AC P01749;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (3).
 OS MUS MUSCULUS (MOUSE).
 OC EDUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE; 81234548.
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 BALTIMORE D.;
 RL CELL 24:625-637(1981).
 CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 DR EMBL; J00536; G554035; -
 DR PIR; A02031; HVMS3.
 DR HSSP; P01810; 1JHL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (3).
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 30 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 85 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 117 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13016 MW; 0F12FC8B CRC32;

Query Match 46.9% Score 447; DB 1; Length 117;
 Best Local Similarity 75.0% Pred. No. 2.6e-35;
 Matches 84; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
 QY 6 VILFVSTATSVHSQVOLVSGAEVKKPGASVSKSGSGYTFSTYMHVWVROAPGQRL 65

DB 6 IILFVATATGVHSQVOLVSGAEVKKPGASVSKSGSGYTFSTYMHVWVROAPGQRL 65
 QY 66 WIGSIDSESTNTNOKFKGVTLTVDISASTAMELSLSRSEDTAVYYCAR 117
 DB 66 WIGNIVPSDETHYNOKFKDATTLVKSSSTAYMDLSRLSDSAVAYCAK 117

RESULT 10
 HV09_MOUSE STANDARD; PRT; 117 AA.
 ID HV09_MOUSE
 AC P01753; P11271;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (186-1).
 OS MUS MUSCULUS (MOUSE).
 OC EDUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE; 81234548.
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 BALTIMORE D.;
 RL CELL 24:625-637(1981).
 CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 DR PIR; B02034; HVMS61.
 DR HSSP; P01810; 1FVB.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (186-1).
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12890 MW; C97683A2 CRC32;

Query Match 46.6% Score 445; DB 1; Length 117;
 Best Local Similarity 72.3% Pred. No. 4e-35;
 Matches 81; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
 QY 6 VILFVSTATSVHSQVOLVSGAEVKKPGASVSKSGSGYTFSTYMHVWVROAPGQRL 65
 DB 6 IILFVATATGVHSQVOLVSGAEVKKPGASVSKSGSGYTFSTYMHVWVROAPGQRL 65
 QY 66 WIGSIDSESTNTNOKFKGVTLTVDISASTAMELSLSRSEDTAVYYCAR 117
 DB 66 WIGRIDPNSGGTNTAPRFGQVTVTRDASFSTAYMDLSRLSDSAVAYCAK 117

RESULT 11
 HV04_MOUSE STANDARD; PRT; 117 AA.
 ID HV04_MOUSE
 AC P01748;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (23).
 OS MUS MUSCULUS (MOUSE).
 OC EDUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE; 81234548.
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 BALTIMORE D.;

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RL CELL 24:625-637(1981).
CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
DR PIR: A02030; HWS23.
DR HSSP: P01810; 1JHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (23).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; 66B34D1A CRC32;

Query Match
Best Local Similarity 46.4%; Score 443; DB 1; Length 117;
Matches 82; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

OY 6 VLFLVSTSTSVHSQVQLVQSGAEVKKPKASVAVSCSGSYTFTSYMMHWVQAPOQRLE 65
DB 6 ILFLVAAANGVHSQVQLVQSGAEVKKPKASVAVSCSGSYTFTSYMMHWVQAPOQRLE 65
OY 66 WIGELDPSSNTNINOKFKGRVTLVDISASTAYMELSLRSEDVAVYICAR 117
DB 66 WIGNINPGNGGINTYNEKFKSKVTLTYDKSSSTRATYLTSLTSDSAVYICAR 117

RESULT 12
HY45_MOUSE STANDARD: PRT; 136 AA.
ID HY45_MOUSE
AC P01759;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (BC11).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82222262.
RA KNAPP M.R., LIU C.-P., NEWELL N., WARD R.B., TUCKER P.W., STROBER S.,
RA BLATTNER F.R.,
RL PROC. NATL. ACAD. SCI. U.S.A. 79:2996-3000(1982).
DR EMBL: J00494; G195011; -.
DR PIR: A02042; HWSB1.
DR HSSP: P01789; 1JHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION (BC11).
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; E04F1C7E CRC32;

Query Match
Best Local Similarity 46.4%; Score 443; DB 1; Length 136;
Matches 87; Conservative 15; Mismatches 27; Indels 8; Gaps 2;

OY 6 VLFLVSTSTSVHSQVQLVQSGAEVKKPKASVAVSCSGSYTFTSYMMHWVQAPOQRLE 65.
DB 6 ILFLVAAANGVHSQVQLVQSGAEVKKPKASVAVSCSGSYTFTSYMMHWVQAPOQRLE 65
OY 66 WIGELDPSSNTNINOKFKGRVTLVDISASTAYMELSLRSEDVAVYICAR--GGYDGM 123
DB 66 WIGVISTYNGNTSYNOKFKGRVTLVDISASTAYMELSLRSEDVAVYICAR--GGYDGM 123
OY 124 DYALDITWGGLTYVSS 140
DB 124 DYALDITWGGLTYVSS 140
OY 123 ---FDYWGGLTYVSS 136
DB 123 ---FDYWGGLTYVSS 136

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RESULT 13
HY50_MOUSE STANDARD: PRT; 120 AA.
ID HY50_MOUSE
AC P06329;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (AC38 15.3).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE: 84182519.
RA DILDROP R., BOVENS J., SIEKEVITZ M., BEYREUTHER K., RAJEWSKY K.;
RL EMBO J. 3:517-523(1984).
DR PIR: A02037; HWS15.
DR HSSP: P01772; 1FGV.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 85EC01BA CRC32;

Query Match
Best Local Similarity 45.9%; Score 437.5; DB 1; Length 120;
Matches 82; Conservative 12; Mismatches 26; Indels 1; Gaps 1;

OY 20 QVQLVQSGAEVKKPKASVAVSCSGSYTFTSYMMHWVQAPOQRLEWIGELDPSSNTIN 79
DB 1 QVQLVQSGAEVKKPKASVAVSCSGSYTFTSYMMHWVQAPOQRLEWIGELDPSSNTIN 79
OY 80 NQKFKGRVTLVDISASTAYMELSLRSEDVAVYICARGGYDGMVAYDITWGGLTYVSS 139
DB 61 NEKFKSKVTLTYDKSSSTRATYLTSLTSDSAVYICARWDYEG-DRYFDYWGGLTYVSS 119
OY 140 S 140
DB 120 S 120

RESULT 14
HY49_MOUSE STANDARD: PRT; 117 AA.
ID HY49_MOUSE
AC P06328;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH558 B4).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85093340.
RA YANCOPOULOS G.D., ALT F.W.;
RL CELL 40:271-281(1985).
DR EMBL: M13788; G456292; -.
DR PIR: A02035; HWSB4.
DR HSSP: P01810; 1JHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (VH558 B4).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.

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FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA: 12834 MW: 85692FE5 CRC32;

Query Match 45.4%; Score 433; DB 1; Length 117;
 Best Local Similarity 70.5%; Pred. No. 5.3e-34;
 Matches 79; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 6 VILFLVSTATSVASOVOLVSGAEVKKPGASVYVSCGSGTFTSYMMHWVROAPGQRL 65
 Db 6 IMFLATATGVSFVQLOQPGAEVKKPGASVYVSCGSGTFTSYMMHWVROAPGQRL 65
 QY 66 WIGELDPSESNTYNNOKFKGRVTLTYDISASTAYMELSLRSEDYAVYCAR 117
 Db 66 WIGNIDPNSGCTYNNKFKSKATLTVDKPSSTAYMOLSLTSEDSAVYCYCR 117

RESULT 15
 HV10_MOUSE
 ID HV10_MOUSE STANDARD; PRT; 117 AA.

AC P01754; P11270;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (145).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE; 81234548.
 RA BOWHILL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 RA BALTIMORE D.;
 RL CELL 24:625-637(1981).
 CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 CC EMBL: J00533; G554033; -.
 DR PIR: C02034; HYMS45.
 DR HSSP: P01810; 1JHL.
 DR HSP: P01810; 1JHL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (145).
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT NON_TER 117
 SQ SEQUENCE 117 AA: 12921 MW: D9E6B000 CRC32;

Query Match 44.8%; Score 427; DB 1; Length 117;
 Best Local Similarity 70.5%; Pred. No. 1.9e-33;
 Matches 79; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 6 VILFLVSTATSVASOVOLVSGAEVKKPGASVYVSCGSGTFTSYMMHWVROAPGQRL 65
 Db 6 IMFLATATGVSFVQLOQPGAEVKKPGASVYVSCGSGTFTSYMMHWVROAPGQRL 65
 QY 66 WIGELDPSESNTYNNOKFKGRVTLTYDISASTAYMELSLRSEDYAVYCAR 117
 Db 66 WIGRIDPNSGCTYNNKFKSKATLTVDKPSSTAYMOLSLTSEDSAVYCYCR 117

Search completed: May 11, 1999, 12:20:08
 Job time: 305 sec

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OM protein - protein search, using sw model

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Run on:      May 11, 1999, 12:21:01 ; Search time 38.54 Seconds .
              (without alignments)
              257.666 Million cell updates/sec
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Title: US-08-700-737-19
Page: 854

Sequence: 1 MKCTWILFLVSTATSHQ.....GTALGCLVKDYFPEPTVS 180

Scoring table: BLOSUM62

Searched: 180763 seqs, 55169189 residues

Database :

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15: SPTREMBL.8:*
14:
13: 1: sp_fungi:*
12: 2: sp_human:*
11: 3: sp_invertebrate:*
10: 4: sp_mammal:*
9: 5: sp_mhc:*
8: 6: sp_organelle:*
7: 7: sp_phage:*
6: 8: sp_plant:*
5: 9: sp_bacteria:*
4: 10: sp_virus:*
3: 11: sp_rodent:*
2: 12: sp_vertebrate:*
1: 13: sp_unclassified:*
0: 14: sp_archaea:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	212	23.3	82	2	075729	075729 homo sapien
2	212	22.2	76	2	075742	075742 homo sapien
3	211.5	22.2	85	2	075724	075724 homo sapien
4	199	20.9	88	2	075737	075737 homo sapien
5	198.5	20.8	77	2	075726	075726 homo sapien
6	198	20.7	77	2	075728	075728 homo sapien
7	197.5	20.7	78	2	075730	075730 homo sapien
8	194	20.3	86	2	075722	075722 homo sapien
9	194	20.3	77	2	075741	075741 homo sapien
10	191.5	20.1	81	2	075719	075719 homo sapien
11	191	20.0	74	2	075744	075744 homo sapien
12	189.5	19.9	81	2	075734	075734 homo sapien
13	189	19.8	78	2	075723	075723 homo sapien
14	188	19.7	86	2	075740	075740 homo sapien
15	186	19.5	72	2	075738	075738 homo sapien
16	185.5	19.4	81	2	075721	075721 homo sapien
17	184	19.3	80	2	075735	075735 homo sapien
18	181.5	19.0	82	2	075725	075725 homo sapien
19	181.5	19.0	80	2	075727	075727 homo sapien
20	181.5	19.0	79	2	075731	075731 homo sapien
21	177	18.6	82	2	075732	075732 homo sapien
22	172.5	18.1	81	2	075736	075736 homo sapien
23	172	18.0	76	2	075739	075739 homo sapien
24	164	17.2	78	2	075733	075733 homo sapien
25	163.5	17.1	97	2	043734	043734 homo sapien
26	159.5	16.7	75	2	075743	075743 homo sapien
27	155	16.2	45	2	076051	076051 homo sapien
28	154	16.1	78	2	075720	075720 homo sapien
29	150.5	15.8	254	12	090537	090537 gnglymstoc

30	138	14.5	64	10	Q615750	Q615750	mus musculus
31	137.5	14.4	258	12	Q905559	Q90559	ginglymasto
32	132	13.8	250	12	Q90569	Q90569	ginglymasto
33	127	13.3	258	12	Q90556	Q90556	ginglymasto
34	126	13.2	119	2	Q99589	Q99589	homo sapien
35	123	12.9	268	12	Q90524	Q90524	ginglymasto
36	121.5	12.7	121	2	Q99600	Q99600	homo sapien
37	120	12.6	265	12	Q90543	Q90543	ginglymasto
38	117.5	12.3	684	12	Q90544	Q90544	ginglymasto
39	116	12.2	145	2	Q16237	Q16237	homo sapien
40	114.5	12.0	38	2	Q15224	Q15224	homo sapien
41	112	11.7	237	12	Q90545	Q90545	ginglymasto
42	111.5	11.7	130	10	P80913	P80913	mus musculus
43	111	11.6	158	12	Q90531	Q90531	ginglymasto
44	109	11.4	257	12	Q90536	Q90536	ginglymasto
45	108	11.3	188	12	Q90528	Q90528	ginglymasto

ALIGNMENTS

```

RESULT 1
075729 ID 075729 PRELIMINARY; PRT; 82 AA.
AC 075729;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
VN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
RL mutated VH region genes."
DR SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
FT EMBL; AJ009526; E1311452; -.
FT NON_TER 1
FT NON_TER 82
FT NON_TER 82
SQ SEQUENCE 82 AA; 9396 MW; 9063B32A CRC32;

Query Match 23.3%; Score 222; DB 2; Length 82;
Best Local Similarity 49.4%; Pred. No. 1.2e-13;
Matches 41; Conservative 15; Mismatches 23; Indels 4; Gaps 2

QY 51 YMHVVRAPGPGORLEWICEIDPSESNTNINCKFKGRVLTVDISASTAYMELSLRSEDT 110
   1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 YAMSVVRAPGPGGLEWISIDAGIDTYAESVKGRFTISRDNRSKNTLYLQNMNTLRAEDT 60
   1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 111 AVYCGAGGYDG--WDYAIDYW 130
   1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 AVYTCVKDGVGSANSYWDY-FDTW 82
   1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
075742 ID 075742 PRELIMINARY; PRT; 76 AA.
AC 075742;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
VN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.

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DT	01-NOV-1998	(TREMELREL. 08, CREATED)
DT	01-NOV-1998	(TREMELREL. 08, LAST SEQUENCE UPDATE)
DT	01-NOV-1998	(TREMELREL. 08, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).	

GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009525; E1311450; -.
 FT NON_TER 1
 FT NON_TER 77
 SQ SEQUENCE 77 AA; 8925 MW; EA14CFDF CRC32;

Query Match 20.8%; Score 198; DB 2; Length 77;
 Best Local Similarity 45.5%; Pred. No. 1.8e-11;
 Matches 35; Conservative 18; Mismatches 20; Indels 4; Gaps 1;

OY 51 YMMHWVROAPGQRLWIGELIDPESNTNMYNOKFKGRVTLTVDISASTAYMELSSLRSED 110
 DB 1 YMMHWVROAPGQRLWIGELIDPESNTNMYNOKFKGRVTLTVDISASTAYMELSSLRSED 60
 OY 111 AVYYCARG---GYDGM 123
 DB 61 ALYYCARGKRGSEFDY 77

RESULT 7
 ID 075730 PRELIMINARY; PRT; 78 AA.
 AC 075730;
 DT 01-NOV-1998 (TREMELREL. 08, CREATED)
 DT 01-NOV-1998 (TREMELREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009527; E1311454; -.
 FT NON_TER 1
 FT NON_TER 78
 SQ SEQUENCE 78 AA; 8994 MW; OA38F0E5 CRC32;

Query Match 20.7%; Score 197.5; DB 2; Length 78;
 Best Local Similarity 46.1%; Pred. No. 2e-11;
 Matches 35; Conservative 16; Mismatches 22; Indels 3; Gaps 1;

OY 51 YMMHWVROAPGQRLWIGELIDPESNTNMYNOKFKGRVTLTVDISASTAYMELSSLRSED 110
 DB 3 YMMHWVROAPGQRLWIGELIDPESNTNMYNOKFKGRVTLTVDISASTAYMELSSLRSED 62
 OY 111 AVYYCARG---GYDGM 123
 DB 63 AVYHCARDVNGHFDY 78

RESULT 8
 ID 075722 PRELIMINARY; PRT; 86 AA.
 AC 075722;
 DT 01-NOV-1998 (TREMELREL. 08, CREATED)

DT 01-NOV-1998 (TREMELREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009519; E1311438; -.
 FT NON_TER 1
 FT NON_TER 86
 SQ SEQUENCE 86 AA; 9769 MW; 5F6AC773 CRC32;

Query Match 20.3%; Score 194; DB 2; Length 86;
 Best Local Similarity 47.1%; Pred. No. 4.7e-11;
 Matches 40; Conservative 13; Mismatches 28; Indels 4; Gaps 2;

OY 50 YMMHWVROAPGQRLWIGELIDPESNTNMYNOKFKGRVTLTVDISASTAYMELSSLRSED 109
 DB 2 SHMKVROAPGQRLWIGELIDPESNTNMYNOKFKGRVTLTVDISASTAYMELSSLRSED 61
 OY 110 TAVYICAA--RGYDGM--YADY 130
 DB 62 TAVYICARDGAAAGTYDGYDGM 86

RESULT 9
 ID 075741 PRELIMINARY; PRT; 77 AA.
 AC 075741;
 DT 01-NOV-1998 (TREMELREL. 08, CREATED)
 DT 01-NOV-1998 (TREMELREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009540; E1311476; -.
 FT NON_TER 1
 FT NON_TER 77
 SQ SEQUENCE 77 AA; 8734 MW; 1E7F9E8E CRC32;

Query Match 20.3%; Score 194; DB 2; Length 77;
 Best Local Similarity 50.0%; Pred. No. 4.1e-11;
 Matches 39; Conservative 11; Mismatches 26; Indels 2; Gaps 1;

OY 53 MHWVROAPGQRLWIGELIDPESNTNMYNOKFKGRVTLTVDISASTAYMELSSLRSED 112
 DB 2 MHWVROAPGQRLWIGELIDPESNTNMYNOKFKGRVTLTVDISASTAYMELSSLRSED 61
 OY 113 YVCARGYDGM--YADY 130
 DB 62 YVCARHYDSSP--DY 77

RESULT 10
 ID 075719

ID 075719 PRELIMINARY; PRT: 81 AA.
 AC 075719;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009516; E1311432; -.
 FT NON_TER 1 1
 FT NON_TER 81 81
 SQ SEQUENCE 81 AA; 9074 MW; 288593C4 CRC32;

Query Match 20.1%; Score 191.5; DB 2; Length 81;
 Best Local Similarity 42.9%; Pred. No. 7.4e-11;
 Matches 36; Conservative 18; Mismatches 25; Indels 5; Gaps 2;

QY 49 TSYNHWYRQAPGRLWIGIDPESNTYNQKFGVTLTVDISASTAYMELSLRSE 108
 DB 1 TSYNHWYRQAPGRLWIGIDPESNTYNQKFGVTLTVDISASTAYMELSLRSE 60
 QY 109 DTAIVYCA--RGYDGMWDYDAIW 130
 DB 61 DTAIVYCA--RGYDGMWDYDAIW 81

RESULT 11
 075744 PRELIMINARY; PRT: 74 AA.
 AC 075744;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009545; E1311444; -.
 FT NON_TER 1 1
 FT NON_TER 74 74
 SQ SEQUENCE 74 AA; 8541 MW; 46693A8A CRC32;

Query Match 20.0%; Score 191; DB 2; Length 74;
 Best Local Similarity 44.3%; Pred. No. 7.4e-11;
 Matches 35; Conservative 12; Mismatches 26; Indels 6; Gaps 1;

QY 52 WMHWYRQAPGRLWIGIDPESNTYNQKFGVTLTVDISASTAYMELSLRSEDTA 111
 DB 2 WMHWYRQAPGRLWIGIDPESNTYNQKFGVTLTVDISASTAYMELSLRSEDTA 61
 QY 112 VYTCARGLWYVYKRISSDSRINYADSVKGRFTISDNKNTLYLQMSLRADTAVY 130
 DB 62 VYTCARGLWYVYKRISSDSRINYADSVKGRFTISDNKNTLYLQMSLRADTAVY 74

RESULT 12
 075734 PRELIMINARY; PRT: 81 AA.
 AC 075734;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009531; E1311462; -.
 FT NON_TER 1 1
 FT NON_TER 81 81
 SQ SEQUENCE 81 AA; 9040 MW; 56B4D902 CRC32;

Query Match 19.9%; Score 189.5; DB 2; Length 81;
 Best Local Similarity 44.4%; Pred. No. 1.1e-10;
 Matches 36; Conservative 14; Mismatches 24; Indels 7; Gaps 1;

QY 50 SYNHWYRQAPGRLWIGIDPESNTYNQKFGVTLTVDISASTAYMELSLRSE 109
 DB 1 SYNHWYRQAPGRLWIGIDPESNTYNQKFGVTLTVDISASTAYMELSLRSE 60
 QY 110 TAVYCAR-----GGYDGM 123
 DB 61 TAVYCAR-----GGYDGM 81

RESULT 13
 075723 PRELIMINARY; PRT: 78 AA.
 AC 075723;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009520; E1311440; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9075 MW; DFEED569 CRC32;

Query Match 19.8%; Score 189; DB 2; Length 78;
 Best Local Similarity 54.0%; Pred. No. 1.2e-10;
 Matches 34; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 55 WYRQAPGRLWIGIDPESNTYNQKFGVTLTVDISASTAYMELSLRSEDTAVY 114
 DB 1 WYRQAPGRLWIGIDPESNTYNQKFGVTLTVDISASTAYMELSLRSEDTAVY 60
 QY 115 CAR 117

Db 61 CAR 63

RESULT 14

ID 075740 PRELIMINARY; PRT: 86 AA.

AC 075740;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.

OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE-INTESTINE;

RA FISCHER M., KUEPPERS R.;

RT "Human IgA and IgM secreting intestinal plasma cells carry heavily

mutated VH region genes."

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ009539; E1311474; -.

FT NON_TER 1 1

FT NON_TER 86 86

SO SEQUENCE 86 AA; 9625 MW; 07627E8C CRC32;

Query Match 19.78; Score 188; DB 2; Length 86;

Best Local Similarity 51.58; Pred. No. 1.7e-10;
Matches 34; Conservative 13; Mismatches 17; Indels 2; Gaps 1;

OY 52 MNWVROAPGKLEWISSTGFIYYTDSVGRGRTTISDIANNVYLQNSLRDDFAV 62

Db 3 MNWVROAPGKLEWISSTGFIYYTDSVGRGRTTISDIANNVYLQNSLRDDFAV 62

OY 110 TAVYYC 115

Db 63 TAVYYC 68

RESULT 15

ID 075738 PRELIMINARY; PRT: 72 AA.

AC 075738;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

GN VH.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE-INTESTINE;

RA FISCHER M., KUEPPERS R.;

RT "Human IgA and IgM secreting intestinal plasma cells carry heavily

mutated VH region genes."

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ009537; E1311470; -.

FT NON_TER 1 1

FT NON_TER 72 72

SO SEQUENCE 72 AA; 8345 MW; E0FB044A CRC32;

Query Match 19.58; Score 186; DB 2; Length 72;

Best Local Similarity 44.98; Pred. No. 2.1e-10;
Matches 35; Conservative 14; Mismatches 21; Indels 8; Gaps 1;

OY 53 MNWVROAPGKLEWISSTGFIYYTDSVGRGRTTISDIANNVYLQNSLRDDFAV 112

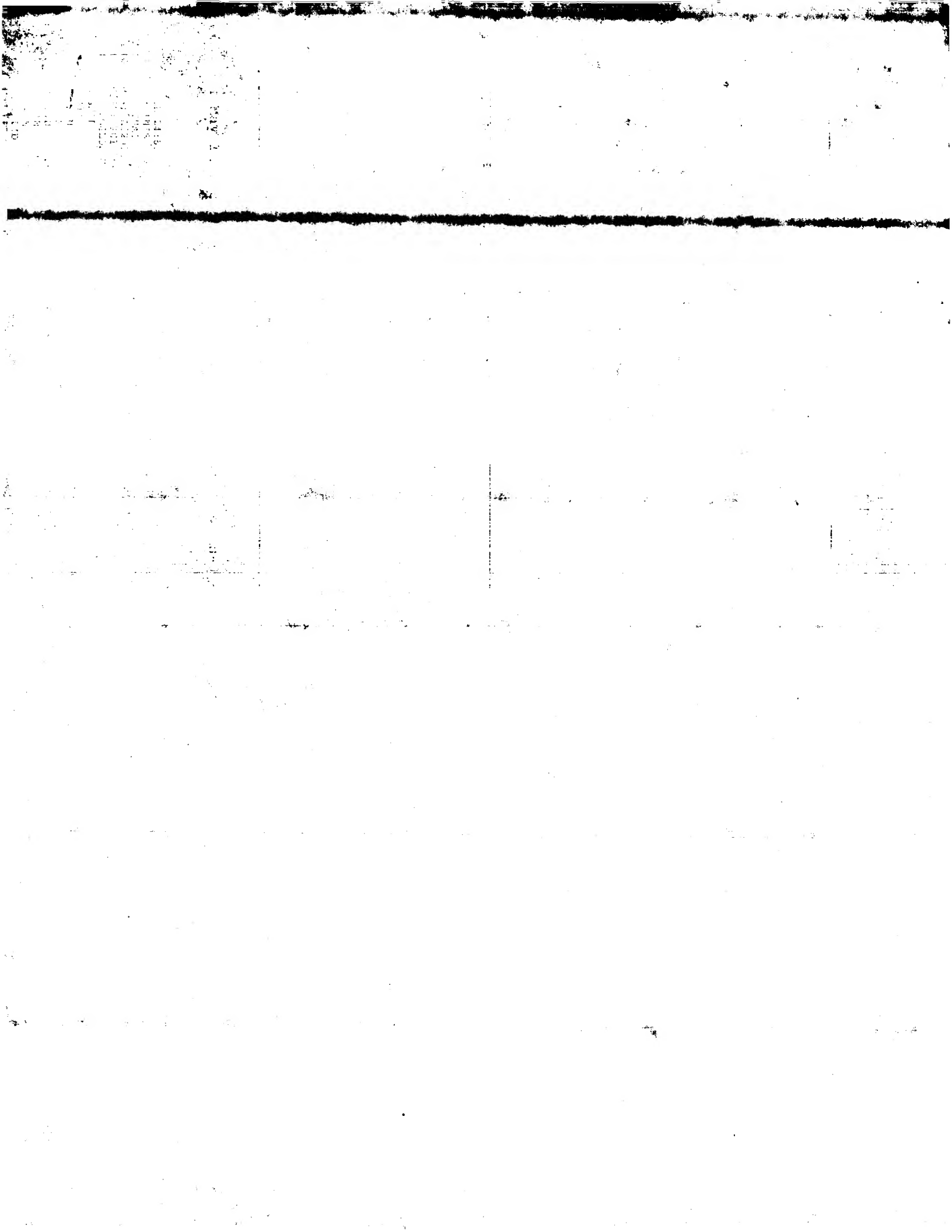
Db 3 MNWVROAPGKLEWISSTGFIYYTDSVGRGRTTISDIANNVYLQNSLRDDFAV 112

Db 3 MNWVROAPGKLEWISSTGFIYYTDSVGRGRTTISDIANNVYLQNSLRDDFAV 62

OY 113 YTCARGGDDMDYALDYW 130

Db 63 YTCARD-----LAW 72

Search completed: May 11, 1999, 12:21:01
Job time: 253 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:14:55 ; Search time 44.09 Seconds
(without alignments)
82.571 Million cell updates/sec

Title: US-08-700-737-19

Perfect score: 954
Sequence: 1 MCTWVILFLVSTATSVHSQ.....GTAALGLVNDYPEPTVS 180

Scoring table: BLOSUM62

Searched: 162880 seqs, 20225328 residues

Database: A_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	951	99.7	180	1	W53813	Heavy chain of a h
2	736.5	77.2	249	1	R77610	Humanised 5G1.1 VH
3	729.5	76.5	249	1	R77615	Humanised 5G1.1 VH
4	727	76.2	652	1	W48650	Heavy chain of hma
5	720.5	75.5	249	1	R77611	Humanised 5G1.1 VH
6	685.5	71.9	481	1	R24442	Sequence of antiho
7	679.5	71.2	279	1	W05846	Humanised M291 ant
8	676	70.9	449	1	R43339	Completely humani
9	676	70.9	222	1	R39267	Humanised CAG1 Ig
10	676	70.9	235	1	R39268	Humanised CAG1 Ig
11	676	70.9	449	1	W49816	Amino acid sequenc
12	676	70.9	222	1	W49817	Fragment of human
13	676	70.9	235	1	W49818	Amino acid sequenc
14	670.5	70.3	468	1	R28808	pre-5A8 humanised
15	669.5	70.2	464	1	W14941	3F4 Human IgG4 exp
16	669.5	70.2	464	1	W14938	Murine anti-porc
17	669.5	70.2	463	1	W14939	3F4 (Chimeric) hum
18	669.5	70.2	463	1	W14940	3F4 (Chimeric) hum
19	668.5	70.1	235	1	R41682	Chimeric antibody c
20	655.5	68.7	249	1	R77609	Chimeric heavy cha
21	651	68.2	476	1	R31023	Antibody D heavy c
22	648.5	68.0	465	1	R66758	Anti-tobacco mosai
23	646.5	67.8	235	1	R41707	Murine 128.1 VH/hu
24	644.5	67.6	235	1	R86324	Anti-IL-8 Mab 6G4.
25	644.5	67.6	253	1	W23791	Chimeric monoclonal
26	644.5	67.6	253	1	W31581	Chimeric anti IL-8
27	644.5	67.6	253	1	W42324	Murine variable re
28	644.5	67.6	253	1	W33766	Chimeric anti IL-8
29	644.5	67.6	253	1	W40127	Chimeric Mab 6G4.2
30	641.5	67.2	233	1	R41710	Murine 128.1 VH/hu
31	641.5	67.2	233	1	R41715	Murine 128.1 VH/hu
32	640	67.1	464	1	R76088	Mab 55.1 heavy cha
33	639	67.0	463	1	W14935	2A2 Human IgG4 exp
34	639	67.0	463	1	W14932	Murine anti-porc
35	639	67.0	462	1	W14933	2A2 (Chimeric) hum
36	639	67.0	462	1	W14934	2A2 (Chimeric) hum
37	639	67.0	236	1	R67436	ORF3 monoclonal an
38	636	66.7	144	1	W53816	Consensus protein
39	635	66.6	140	1	W53815	Murine Act-1 heavy
40	623	65.3	137	1	W53818	Protein sequence o
41	619	64.9	468	1	R13061	Monoclonal antibody
42	614	64.4	230	1	W07529	Anti-HGF receptor
43	613	64.3	466	1	R40750	Sequence encoded b

ALIGNMENTS

44	612.5	64.2	552	1	R30775	PH52-8.0 humanised
45	609	63.8	588	1	W71880	Anti-human Fas hum

ALIGNMENTS

RESULT	1	
ID	W53813	standard; Protein; 180 AA.
AC	W53813;	
DE	14-JUL-1998	(first entry)
DE	Heavy chain of a humanised murine Act-1 antibody.	
KW	Mouse; Act-1 antibody; human alpha4-beta7 integrin;	
KW	Mucosal addressin cell adhesion molecule-1; MacCAM-1;	
KW	humanised antibody; murine antigen binding region; inhibition	
KW	leukocyte infiltration of tissue; treatment; inflammatory disease;	
KW	inflammatory bowel disease.	
OS	Synthetic.	
OS	Mus sp.	
OS	Homo sapiens.	
EH	Key	Location/Qualifiers
FT	Peptide	1..19
FT		/note="signal peptide"
FT	Protein	20..180
FT		/note="mature protein"
PN	W09806248-A2.	
PD	19-FEB-1998.	
PF	06-AUG-1997; U13884.	
PR	15-AUG-1996; US-700737.	
PR	(LEUK-) LEUKOSITE INC.	
PI	Bendig MM, Jones ST, Newman W, Ponath PD, Rindler DJ,	
PI	Saldanha J;	
DR	WPI; 98-159172/14.	
DR	N-PSDB; V20076.	
PT	Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -	
PT	used for treating inflammatory disease, pancreatitis, diabetes,	
PT	asthma, graft versus host disease and sarcoidosis	
PS	Claim 20; Fig 11, 145pp; English.	
CC	The present sequence represents the heavy chain of humanised murine	
CC	antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.	
CC	Mucosal addressin cell adhesion molecule-1 (MacCAM-1) is a ligand of	
CC	this particular integrin. The Act-1 antibody interferes with alpha4-beta7	
CC	integrin binding to MacCAM-1, which is present of high endothelial	
CC	venules in mucosal lymph nodes. The humanised immunoglobulin can be	
CC	used to inhibit the interaction of cells bearing alpha4-beta7 with	
CC	cells bearing a ligand for alpha4-beta7. It can be used for inhibiting	
CC	leukocyte infiltration of tissues, e.g. for treating inflammatory	
CC	diseases such as inflammatory bowel disease. The immunoglobulin can	
CC	also be used for detection, isolation and diagnosis.	
CC	Sequence 180 AA;	
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AC R77610; (first entry)
 DE 15-MAR-1996 (first entry)
 DE Humanised 5G1.1 VH + IGHRL.
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR.
 OS Synthetic.
 FH Key
 FT peptide
 FT 1.19
 FT /label= sig_peptide
 FT 20.249
 FT /label= mat_peptide
 FT 45.34
 FT /label= CDR-H1
 FT 69.79
 FT /label= CDR-H2
 FT 118.130
 FT /label= CDR-H3
 FT region
 FT WO9529697-A1.
 PN 09-NOV-1995.
 PD 01-MAY-1995; U05688.
 PF 02-MAY-1994; US-236208.
 PR (ALEX-) ALEXION PHARM INC.
 PA Evans MJ, Mattis L, Mueller EE, Nye SH, Rollins S;
 PI Rothen RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 PI WPI: 95-392923/50.
 DR N-PSDB: T08483.
 PT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 PS Example 11; Page 119-122; 181pp; English.
 CC A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH
 CC + IGHRL (R77610), includes CDRs derived from mouse anti-C5 monoclonal
 CC antibody 5G1.1. It can be co-expressed with a humanised light
 CC chain (R77612) in human 293 EBNA cells using encoding DNAs
 CC subcloned into vector APEX-3p (T08476). Such humanised recombinant
 CC antibodies retain the ability of Mab 5G1.1 to block human complement
 CC C5a generation and thus to reduce glomerular inflammation and kidney
 CC dysfunction associated with glomerulonephritis.
 SQ Sequence 249 AA;

Query Match 77.28; Score 736.5; DB 1; Length 249;
 Best Local Similarity 78.7%; Pred. No. 2.3e-49;
 Matches 144; Conservative 10; Mismatches 24; Indels 5; Gaps 2;

QY 1 MKCTWVILFLVSTATSHVSOVLQVSGAEVKKRPGASVYVSCKSGYTFSTYMMHWVROAP 60
 DB 1 MKMSWVILFLVSTVAGVHSGVQLVQSGAEVKKRPGASVYVSCKSGYTFSTYMMHWVROAP 60
 QY 61 GORLEWIGEIDPSESNNTYNNQKFGKRVTLVDISASTAYMELSLRSEDTAVYYCAR---118
 DB 61 GQGLEWMEGELIPGSGSTFYAKRFGKRVMTADTSTSTAYMELSLRSEDTAVYYCARFF 120
 QY 118 GGYGWDYDAIDYWGQGLTVVSSASTKGPVFPPLAPSSKSTSGGTALGCLVNDYFPEPV 177
 DB 121 GSSPNWYF--DVWGQGLTVVSSASTKGPVFPPLAPSSKSTSGGTALGCLVNDYFPEPV 178
 QY 178 TVS 180
 DB 179 TVS 181

RESULT 3
 ID R77615 standard; Protein; 249 AA.
 AC R77615;
 DE 02-APR-1996 (first entry)
 DE Humanised 5G1.1 VH + IGHRL.
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR.
 OS Synthetic.

FH Key
 FT peptide
 FT 1.19
 FT /label= sig_peptide
 FT 20.249
 FT /label= mat_peptide
 FT 45.34
 FT /label= CDR-H1
 FT 69.79
 FT /label= CDR-H2
 FT 118.130
 FT /label= CDR-H3
 FT region
 FT WO9529697-A1.
 PN 09-NOV-1995.
 PD 01-MAY-1995; U05688.
 PF 02-MAY-1994; US-236208.
 PR (ALEX-) ALEXION PHARM INC.
 PA Evans MJ, Mattis L, Mueller EE, Nye SH, Rollins S;
 PI Rothen RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 PI WPI: 95-392923/50.
 DR N-PSDB: T08487.
 PT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 PS Claim 37; Pages 135-137; 181pp; English.
 CC A DNA construct (T08487) codes for a humanised CDR-grafted
 CC light chain, designated 5G1.1 VL + IGHRLD (R77615), which includes
 CC CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The
 CC DNA can be subcloned together with DNA (T08484) coding
 CC for a humanised Fd (R77611) into vector APEX-3p (T08476) for
 CC expression of humanised antibody in human 293 EBNA cells. Such
 CC recombinant antibodies retain the ability of Mab 5G1.1 to block
 CC human complement C5a generation and thus to reduce glomerular
 CC inflammation and kidney dysfunction associated with
 CC glomerulonephritis.
 SQ Sequence 249 AA;

Query Match 76.5%; Score 729.5; DB 1; Length 249;
 Best Local Similarity 78.1%; Pred. No. 7.7e-49;
 Matches 143; Conservative 10; Mismatches 25; Indels 5; Gaps 2;

QY 1 MKCTWVILFLVSTATSHVSOVLQVSGAEVKKRPGASVYVSCKSGYTFSTYMMHWVROAP 60
 DB 1 MKMSWVILFLVSTVAGVHSGVQLVQSGAEVKKRPGASVYVSCKSGYTFSTYMMHWVROAP 60
 QY 61 GORLEWIGEIDPSESNNTYNNQKFGKRVTLVDISASTAYMELSLRSEDTAVYYCAR---118
 DB 61 GQGLEWMEGELIPGSGSTFYAKRFGKRVMTADTSTSTAYMELSLRSEDTAVYYCARFF 120
 QY 118 GGYGWDYDAIDYWGQGLTVVSSASTKGPVFPPLAPSSKSTSGGTALGCLVNDYFPEPV 177
 DB 121 GSSPNWYF--DVWGQGLTVVSSASTKGPVFPPLAPSSKSTSGGTALGCLVNDYFPEPV 178
 QY 178 TVS 180
 DB 179 TVS 181

RESULT 4
 ID W48650 standard; Protein; 652 AA.
 AC W48650;
 DE 04-AUG-1998 (first entry)
 DE Heavy chain of hmb425 fused to TNF alpha.
 KW Antibody-cytokine fusion protein; tristicronic vector; chimeric;
 KW TNF alpha; IL-2; IRES; Internal ribosome entry site.
 OS Synthetic.
 FH Key
 FT Region
 FT 1.494
 FT /note="Heavy chain of human mab 425"
 FT 495.652
 FT /note="TNF alpha"
 FT Region
 FT WO9811241-A1.
 PN 19-MAR-1998.
 PD 02-SEP-1997; E04765.
 PR 30-SEP-1996; EP-115635.
 PR 16-SEP-1996; EP-114820.
 PA (MERE) MERCK PATENT GMBH.

PI Bruemmer W, Burge C, Dunker R, Hauser H, Mielke C,
 PI Rieke E, von Hoegen I, Welge T;
 DR WPI: 98-207400/18.
 DR N-PSDB: V18096.
 PT Oligo: cistronic expression vector - useful for production of, e.g.
 PS Mab425/TNF- α or Mab425/IL-2 antibody fusion protein
 CC Disclosure: Fig 15; 89pp; English.
 CC The present sequence represents a fusion protein comprising of TNF
 CC alpha fused to the C-terminus of the heavy chain of the human
 CC monoclonal antibody 425 (hmb425). The hmb425 has specificity for
 CC the human EGF receptor. The invention claims for a new pMCDHAP
 CC tricistronic vector (V18096) for the expression of an antibody-cytokine
 CC fusion protein, hmb425-TNF alpha. The TNF alpha sequence can be
 CC substituted by the IL-2 sequence. The vector also contains a strong
 CC promoter/enhancer unit, a selection marker gene and at least two
 CC poliovirus derived internal ribosomal entry site (IRES) sequences. The
 CC vector can be expressed in mammalian host cells for the production of
 CC heteromeric fusion proteins. This expression system is claimed to
 CC produce the heteromeric proteins in high yields.
 SQ Sequence 652 AA;

Query Match 76.2%; Score 727; DB 1; Length 652;

Best Local Similarity 70.1%; Pred. No. 3.2e-48; Mismatches 28; Indels 24; Gaps 1;

Matches 143; Conservative 9; Mismatches 28; Indels 24; Gaps 1;

QY 1 MCKTWLFLVSTATSHSOVOLVQSGAEVKKPGASVKSCKSGYFTSYMMHWQAP 60
 Db 1 MDWTWYFCLLAVALPAGHSQLVQSGAEVKKPGASVKSCKSGYFTSYMMHWQAP 60
 QY 61 GQRLWIGELIDPSEBNTNNQKFKGRTLVVDISASTAYMELSLRSEDYAVVYCAR 120
 Db 61 GQGLEWIGELIDPSEBNTNNQKFKGRTLVVDISASTAYMELSLRSEDYAVVYCAR 120
 QY 121 DGMWDYALDYGQGLTVVSS-----ASRKGSPVEPLAASR 156
 Db 121 DYGRFRFDYWGQGLTVVSSGEMILCAWALCPTPRSHGTTSLAATKGPVPLAPSSK 180
 QY 157 STSGTAAAGCLVKDYFPEPVTVS 180
 Db 181 STSGTAAAGCLVKDYFPEPVTVS 204

RESULT 5
 ID R77611 standard: Protein; 249 AA.
 AC R77611:
 DT 02-APR-1996 (first entry)
 DE Humanised 5G1.1 VH + IGHR.LC.
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KM monoclonal antibody; antiinflammatory; antibody engineering;
 OS humanised antibody; complementarity determining region; CDR.
 FH Synthetic.
 FT key Location/Qualifiers
 FT peptide 1..19
 FT /label= sig_peptide
 FT 20..249
 FT /label= mat_peptide
 PN WO9529697-A1.
 PD 09-NOV-1995.
 PF 01-MAY-1995; 005688.
 PR 02-MAY-1994; US-236208.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Mattis L, Mueller EE, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinco SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 DR N-PSDB: T08484.
 DR WPI: 95-392923/50.
 PT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 PS Claim 38; Page 123-125; 181pp; English.
 CC A DNA construct (T08483) codes for a humanised CDR-grafted and
 CC framework sequence-altered Fd 5G1.1 VH + IGHR.L (R77610), which

CC Includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.
 CC The DNA can be subcloned together with DNA (T08484) coding for a
 CC humanised light chain (R77612) into vector APEX-3P (T08476) for
 CC expression of humanised antibody in human 293 EBNA cells. Such
 CC recombinant antibodies retain the ability of Mab 5G1.1 to block
 CC human complement C5a generation and thus to reduce glomerular
 CC inflammation and kidney dysfunction associated with
 CC glomerulonephritis.
 SQ Sequence 249 AA;

Query Match 75.5%; Score 720.5; DB 1; Length 249;

Best Local Similarity 77.0%; Pred. No. 3.7e-48; Mismatches 27; Indels 5; Gaps 2;

QY 1 MCKTWLFLVSTATSHSOVOLVQSGAEVKKPGASVKSCKSGYFTSYMMHWQAP 60
 Db 1 MCKTWLFLVSTATSHSOVOLVQSGAEVKKPGASVKSCKSGYFTSYMMHWQAP 60
 QY 61 GQRLWIGELIDPSEBNTNNQKFKGRTLVVDISASTAYMELSLRSEDYAVVYCAR 118
 Db 61 GQGLEWIGELIDPSEBNTNNQKFKGRTLVVDISASTAYMELSLRSEDYAVVYCAR 120
 QY 118 GQIDWDYALDYGQGLTVVSSASTKGPVFPPLAPSSKSTSGTAAAGCLVKDYFPEPV 177
 Db 121 GSSPNWYF--DVMGQGLTVVSSASTKGPVFPPLAPSSKSTSGTAAAGCLVKDYFPEPV 178
 QY 178 TVS 180
 Db 179 TVS 181

RESULT 6
 ID R24442 standard: Protein; 481 AA.
 AC R24442;
 DT 02-JAN-1992 (first entry)
 DE Sequence of antibody molecule IgG1.
 KW Antibody; immunoglobulin G1.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 308
 FT /label= N
 FT /note= "Substn. to create glycan addition site"
 FT misc_difference 310
 FT /label= S
 FT /note= "see above"
 FT misc_difference 321
 FT /label= N
 FT /note= "see above"
 FT misc_difference 329
 FT /label= N
 FT /note= "see above"
 FT misc_difference 331
 FT /label= S
 FT /note= "see above"
 FT misc_difference 356
 FT /label= N
 FT /note= "see above"
 FT misc_difference 369
 FT /label= N
 FT /note= "see above"
 PN WO9209293-A.
 PD 11-JUN-1992.
 PF 18-NOV-1991; 008605.
 PR 23-NOV-1990; US-618314.
 PA (GEHO) GEN HOSPITAL CORP.
 PI Seed B, Walz G;
 DR N-PSDB: Q25443.
 DR WPI: 92-216789/26.
 PT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
 PT - used in treating chronic inflammation, rheumatoid arthritis,
 PT psoriasis, etc.

PS Disclosure; Fig 1; 46pp; English.
 CC The IgG1, in its nascent form, bears no sialyl-Tex side chains. The
 CC inventors designed a molecule including several such sites for
 CC attachment of sialyl-Tex side chains (see R2442, Fig). The
 CC additional N-linked glycosylation sites are introduced at locations
 CC which impair complement fixing and Fc receptor binding ability. They
 CC are preferably located in the CH2 region of the Ig molecule.
 CC Antibodies bearing multiple sialyl-Tex determinants are useful for
 CC disrupting undesirable interactions between cells or proteins.
 CC Disrupting this interaction has therapeutic applications, for
 CC example, in minimizing inflammation following tissue injury.
 SQ Sequence 481 AA;

Query Match 71.9%; Score 685.5; DB 1; Length 481;
 Best Local Similarity 74.7%; Pred. No. 3.3e-45;
 Matches 142; Conservative 9; Mismatches 26; Indels 13; Gaps 4;
 QY 1 MKCTW-VILELVSTATSVHSGVQLVQSGAEYKKRPGASVKSCCKSGTFTSYMMHWYRQA 59
 DB 5 MDWTRFLFEVVAATGVQSVQLVQSGAEYKKRPGASVKSCCKSGTFTSYMMHWYRQA 64
 QY 60 PGQRLKEIGEDPSESNTNWKRGKRYTLVNDISASTAVMELSLSEDTAVYTCAR-- 118
 DB 65 PGQGLEWGGIIPFGTANAKQKFGKRYTLADESTAYMELSLSEDTAVYTCARDN 124
 QY 118 ----GG--YDGMDAIDYWGQGLTVYSSASTKGPVFPPLAPSSKSTSGGTALGCLVK 170
 DB 125 GAYCGSGGSCSGW---FDPMGQGLTVYSSASTKGPVFPPLAPSSKSTSGGTALGCLVK 181
 QY 171 DYPEPEPTVS 180
 DB 182 DYPEPEPTVS 191

RESULT 7
 W05826
 ID W05826 standard; Protein: 279 AA.
 AC W05826;
 DT 27-JAN-1997 (first entry)
 DE Humanised M291 antibody heavy chain.
 KW CD3 antigen; humanised antibody; bispecific antibody;
 KW B-cell lymphoma; myeloma; leukaemia; hybridoma;
 OS Chimeric Homo sapiens;
 FH Key location/Qualifiers
 FT domain 1..120
 FT region /label= variable-domain
 FT region 31..35
 FT region /label= CDR1
 FT region 50..66
 FT region /label= CDR2
 FT region 79..109
 FT region /label= CDR3
 FT misc-difference 30
 FT /note= "human framework residue 30 is subst. by
 FT equivalent murine framework residue"
 FT misc-difference 44
 FT /note= "human framework residue 44 is subst. by
 FT equivalent murine framework residue"
 FT misc-difference 67
 FT /note= "human framework residue 67 is subst. by
 FT equivalent murine framework residue"
 FT misc-difference 68
 FT /note= "human framework residue 68 is subst. by
 FT equivalent murine framework residue"
 FT misc-difference 70
 FT /note= "human framework residue 70 is subst. by
 FT equivalent murine framework residue"
 FT misc-difference 72
 FT /note= "human framework residue 72 is subst. by
 FT equivalent murine framework residue"

FT misc-difference 74
 FT /note= "human framework residue 74 is subst. by
 FT equivalent murine framework residue"
 FT domain 121..218
 FT /label= CH1_domain
 FT domain 219..238
 FT /label= Hinge_domain
 FT domain 239..279
 FT /label= Fc-1eucine zipper
 W0626964-A1.
 PD 06-SEP-1996.
 PE 29-FEB-1996: U02754.
 PR 01-MAR-1995: US-397411.
 PA (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
 PI (PROT-) PROTEIN DESIGN LABS INC.
 DR Gingrich R, Link BK, Tso JY, Weiner G;
 WPI: 96-412742/41.
 PT New bispecific antibody reactive with both T or NK cells and
 PT malignant B cells - also their humanised forms and hybridomas
 PT producing them, useful for treating or preventing leukaemia,
 PT lymphoma and myeloma
 PS Claim 28; Fig 5d; 85pp; English.
 CC The humanised M291 antibody heavy chain (W05826) includes a
 CC variable region (see also W05825) consisting of human HF2-1/17
 CC heavy chain variable region framework and complementarily
 CC determining regions from the murine M291 antibody specific for CD3
 CC antigen. It can be coexpressed with humanised M291 light chain (see
 CC also W05830) in mammalian host cells. Bispecific antibodies can
 CC be constructed that include a first binding fragment comprising
 CC humanised M291 heavy and light chain variable regions, and a second
 CC binding fragment comprising humanised ID10 heavy and light chain
 CC variable regions (see also W05828-29). Such antibodies are reactive
 CC with both T or NK cells and malignant B cells, and have therapeutic
 CC and diagnostic aplns.
 SQ Sequence 279 AA;

Query Match 71.2%; Score 679.5; DB 1; Length 279;
 Best Local Similarity 83.3%; Pred. No. 5.5e-45;
 Matches 135; Conservative 5; Mismatches 19; Indels 3; Gaps 2;
 QY 20 QVQLVQSGAEYKKRPGASVKSCCKSGTFTSYMMHWYRQAPGQRLKEIGEDPSESNTN 79
 DB 1 QVQLVQSGAEYKKRPGASVKSCCKSGTFTSYMMHWYRQAPGQLEWGGIIPFGTANAKQK 60
 QY 80 NQKFKRGVTLVNDISASTAVMELSLSEDTAVYTCAR--YDGMDAIDYWGQGLTVY 138
 DB 61 NQKFKRGVTLVNDISASTAVMELSLSEDTAVYTCARSAV--YDGMDAIDYWGQGLTVY 118
 QY 139 SSASTKGPVFPPLAPSSKSTSGGTALGCLVKDYPEPEPTVS 180
 DB 119 SSASTKGPVFPPLAPSSKSTSGGTALGCLVKDYPEPEPTVS 160
 RESULT 8
 R43339
 ID R43339 standard; Protein: 449 AA.
 AC R43339;
 DT 29-NOV-1993 (first entry)
 DE Completely humanised C4G1 Ig heavy chain.
 KW Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIb;
 KW monoclonal antibody; platelet agglutination; humanised antibody.
 OS Synthetic.
 PN W09313133-A.
 PD 08-JUL-1993.
 PE 15-DEC-1992: J01630.
 PR 20-DEC-1991: US-812111.
 PR 09-JUN-1992: US-895952.
 PR 11-SEP-1992: US-944159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 PI Co MS, Tso JY;
 WPI: 93-227275/28.

PT Compn. contg. immunoglobulin specific for the GP-IIb and -IIIa
 PT protein - for treating disorders related to vascular thrombosis
 PS Claim 26; Fig 5C; 54pp; Japanese.
 CC This is the sequence of the humanised C4G1 immunoglobulin heavy
 CC chain fragment. See R4338 for the light chain sequence. The
 CC antibody is specific for the platelet membrane glycoprotein
 CC GPIIb/IIIa and inhibits platelet agglutination. The Ig is thus
 CC useful in the treatment of thrombosis.
 SQ Sequence 449 AA;

Query Match 70.9%; Score 676; DB 1; Length 449;
 Best Local Similarity 82.8%; Pred. No. 1.0e-44;
 Matches 135; Conservative 6; Mismatches 16; Indels 6; Gaps 3;

QY 20 QVOLVSGAEVKKPGASVKSCSGYTFSTYMMHWYRQAPGQRLWIGELIDPSESNTNY 79
 ||||||| :
 DB 1 QVOLVSGAEVKKPGSSSVKSCASGYAFITYLEWYRQAPGQRLWIGVITPPSGGNTY 60
 QY 80 NQKFGAVTLTVDISASTAVNELSLRSEDTAVYYCAR--GGYDGMWYADYWGQGLTY 137
 ||||||| :
 DB 61 NEKFKGAVTLTVDISTAVNELSLRSEDTAVYFCARQDNT--GM--FAVWGQGLTY 116
 QY 138 VSSASTKGPSVFPLAPSSKSTSGGTALGCLVKRYFPEPTVS 180
 ||||||| :
 DB 117 VSSASTKGPSVFPLAPSSKSTSGGTALGCLVKDYFPEPTVS 159

RESULT 9
 R39267
 ID R39267 standard; Protein; 222 AA.
 AC R39267;
 DT 29-NOV-1993 (first entry)
 DE Humanised C4G1 Ig heavy-chain Fab fragment.
 KM Immunoglobulin: H-chain; platelet membrane glycoprotein: GPIIb/IIIa;
 OS monoclinal antibody; platelet agglutination; humanised antibody.
 FH Synthetic.
 FT key
 FT region 31..35
 FT region /label= complementarity_determining_region_1
 FT region 50..66
 FT region /label= CDR_2
 FT region 99..108
 FT region /label= CDR_3
 PN MO9313133-A.
 PD 08-JUL-1993.
 PF 15-DEC-1992; J01630.
 PR 20-DEC-1991; US-812111.
 PR 09-JUN-1992; US-895952.
 PR 11-SEP-1992; US-944159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 PI Co MS. Tso JY.
 DR WPI; 93-227275/28.
 PT Compn. contg. immunoglobulin specific for the GP-IIb and -IIIa
 PT protein - for treating disorders related to vascular thrombosis
 PS Disclosure; Fig 7C; 54pp; Japanese.
 CC This is the sequence of the humanised C4G1 immunoglobulin heavy
 CC chain Fab fragment. See R39268 for the Fab'2 sequence. The
 CC antibody is specific for the platelet membrane glycoprotein
 CC GPIIb/IIIa and inhibits platelet agglutination. The Ig is thus
 CC useful in the treatment of thrombosis.
 SQ Sequence 222 AA;

Query Match 70.9%; Score 676; DB 1; Length 222;
 Best Local Similarity 82.8%; Pred. No. 8e-45;
 Matches 135; Conservative 6; Mismatches 16; Indels 6; Gaps 3;

QY 20 QVOLVSGAEVKKPGASVKSCSGYTFSTYMMHWYRQAPGQRLWIGELIDPSESNTNY 79
 ||||||| :
 DB 1 QVOLVSGAEVKKPGSSSVKSCASGYAFITYLEWYRQAPGQRLWIGVITPPSGGNTY 60

QY 80 NQKFGAVTLTVDISASTAVNELSLRSEDTAVYYCAR--GGYDGMWYADYWGQGLTY 137
 ||||||| :
 DB 61 NEKFKGAVTLTVDISTAVNELSLRSEDTAVYFCARQDNT--GM--FAVWGQGLTY 116
 QY 138 VSSASTKGPSVFPLAPSSKSTSGGTALGCLVKRYFPEPTVS 180
 ||||||| :
 DB 117 VSSASTKGPSVFPLAPSSKSTSGGTALGCLVKDYFPEPTVS 159

RESULT 10
 R39268
 ID R39268 standard; Protein; 235 AA.
 AC R39268;
 DT 29-NOV-1993 (first entry)
 DE Humanised C4G1 Ig heavy-chain Fab'2 fragment.
 KM Immunoglobulin: H-chain; platelet membrane glycoprotein: GPIIb/IIIa;
 KM monoclinal antibody; platelet agglutination; humanised antibody.
 OS Synthetic.
 FH key
 FT region 31..35
 FT region /label= complementarity_determining_region_1
 FT region 50..66
 FT region /label= CDR_2
 FT region 99..108
 FT region /label= CDR_3
 PN MO9313133-A.
 PD 08-JUL-1993.
 PF 15-DEC-1992; J01630.
 PR 20-DEC-1991; US-812111.
 PR 09-JUN-1992; US-895952.
 PR 11-SEP-1992; US-944159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 PI Co MS. Tso JY.
 DR WPI; 93-227275/28.
 PT Compn. contg. immunoglobulin specific for the GP-IIb and -IIIa
 PT protein - for treating disorders related to vascular thrombosis
 PS Disclosure; Fig 7D; 54pp; Japanese.
 CC This is the sequence of the humanised C4G1 immunoglobulin heavy
 CC chain Fab'2 fragment. See R39267 for the Fab sequence. The
 CC antibody is specific for the platelet membrane glycoprotein
 CC GPIIb/IIIa and inhibits platelet agglutination. The Ig is thus
 CC useful in the treatment of thrombosis.
 SQ Sequence 235 AA;

Query Match 70.9%; Score 676; DB 1; Length 235;
 Best Local Similarity 82.8%; Pred. No. 8.5e-45;
 Matches 135; Conservative 6; Mismatches 16; Indels 6; Gaps 3;

QY 20 QVOLVSGAEVKKPGASVKSCSGYTFSTYMMHWYRQAPGQRLWIGELIDPSESNTNY 79
 ||||||| :
 DB 1 QVOLVSGAEVKKPGSSSVKSCASGYAFITYLEWYRQAPGQRLWIGVITPPSGGNTY 60
 QY 80 NQKFGAVTLTVDISASTAVNELSLRSEDTAVYYCAR--GGYDGMWYADYWGQGLTY 137
 ||||||| :
 DB 61 NEKFKGAVTLTVDISTAVNELSLRSEDTAVYFCARQDNT--GM--FAVWGQGLTY 116
 QY 138 VSSASTKGPSVFPLAPSSKSTSGGTALGCLVKRYFPEPTVS 180
 ||||||| :
 DB 117 VSSASTKGPSVFPLAPSSKSTSGGTALGCLVKDYFPEPTVS 159

RESULT 11
 W49816
 ID W49816 standard; Protein; 449 AA.
 AC W49816;
 DT 24-SEP-1998 (first entry)
 DE Amino acid sequence of the humanised antibody C4G1 heavy chain.
 KM Humanised antibody C4G1; heavy chain; humanised; immunoglobulin; Ig;
 KM mouse C4G1; antibody; inhibition; antigen; cardiovascular disease;
 KM thromboembolic disorder; cancer; acute myocardial infarction;
 KM unstable angina; stroke; transient ischemic episode; pulmonary embolism;

KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 PN US5777085-A.
 PD 07-JUL-1998.
 PF 17-MAY-1995; 458516.
 PR 03-MAY-1993; US-053159.
 PR 20-DEC-1991; US-812111.
 PR 09-JUN-1992; US-895952.
 PR 11-SEP-1992; US-944159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Co MS, Tso JY;
 DR WPI; 98-398136/34.
 PT New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4g1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
 PS Claim 4; Fig 5D; 35pp; English.
 CC This is the amino acid sequence of the humanised antibody C4g1 heavy chain, used in the method of the invention involving the creation of a humanised immunoglobulin (Ig) derived from the mouse C4g1 antibody. The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute myocardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer cells which develop GPIIb/IIIa on their surfaces, for the detection of GPIIb/IIIa antigens or for isolating platelets.
 CC Sequence 449 AA;

Query Match 70.9%; Score 676; DB 1; Length 449;
 Best Local Similarity 82.8%; Pred. No. 1.6e-44;
 Matches 135; Conservative 6; Mismatches 16; Indels 6; Gaps 3;

QY 20 QVQLVSGAEYKRRGASVYKSCSGSTFTSYMMHWRAQAPGQLEWIGELDPESESTNTY 79
 DB 1 QVQLVSGAEYKRRGASVYKSCSGSTFTSYMMHWRAQAPGQLEWIGVTPSSGCTNY 60
 QY 80 NQKRGRTLVDSASTAVMELSLRSEDPAYVYCAR--GGYGMWDYADYMGQGLTY 137
 DB 61 NEKRGRTLVDSASTAVMELSLRSEDPAYVYCAR--GGYGMWDYADYMGQGLTY 116
 QY 138 VSSASTKGPVYFPLAPSSKSTSGTALGCLVKDYFPEPTVTS 180
 DB 117 VSSASTKGPVYFPLAPSSKSTSGTALGCLVKDYFPEPTVTS 159

RESULT 12
 ID W49817
 AC W49817 standard; Protein; 222 AA.
 DT 24-SEP-1998 (first entry)
 DE Fragment of humanised antibody C4g1 heavy chain.
 KW Humanised antibody C4g1; heavy chain; humanised; immunoglobulin; Ig;
 KW mouse C4g1; antibody; inhibition; antigen; cardiovascular disease;
 KW thromboembolic disorder; cancer; acute myocardial infarction;
 KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;
 KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 PN US5777085-A.
 PD 07-JUL-1998.
 PF 17-MAY-1995; 458516.
 PR 03-MAY-1993; US-053159.
 PR 20-DEC-1991; US-812111.
 PR 09-JUN-1992; US-895952.
 PR 11-SEP-1992; US-944159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Co MS, Tso JY;
 DR WPI; 98-398136/34.
 PT New humanised immunoglobulin which binds GPIIb/IIIa - derived from

PT mouse C4g1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
 PS Disclosure; Fig 7C; 35pp; English.
 CC This is the amino acid sequence of a fragment of humanised antibody C4g1 heavy chain, used in the method of the invention involving the creation of a humanised immunoglobulin (Ig) derived from the mouse C4g1 antibody. The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute myocardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer cells which develop GPIIb/IIIa on their surfaces, for the detection of GPIIb/IIIa antigens or for isolating platelets.
 CC Sequence 222 AA;

Query Match 70.9%; Score 676; DB 1; Length 222;
 Best Local Similarity 82.8%; Pred. No. 8e-45;
 Matches 135; Conservative 6; Mismatches 16; Indels 6; Gaps 3;

QY 20 QVQLVSGAEYKRRGASVYKSCSGSTFTSYMMHWRAQAPGQLEWIGELDPESESTNTY 79
 DB 1 QVQLVSGAEYKRRGASVYKSCSGSTFTSYMMHWRAQAPGQLEWIGVTPSSGCTNY 60
 QY 80 NQKRGRTLVDSASTAVMELSLRSEDPAYVYCAR--GGYGMWDYADYMGQGLTY 137
 DB 61 NEKRGRTLVDSASTAVMELSLRSEDPAYVYCAR--GGYGMWDYADYMGQGLTY 116
 QY 138 VSSASTKGPVYFPLAPSSKSTSGTALGCLVKDYFPEPTVTS 180
 DB 117 VSSASTKGPVYFPLAPSSKSTSGTALGCLVKDYFPEPTVTS 159

RESULT 13
 ID W49818
 AC W49818 standard; Protein; 235 AA.
 DT 24-SEP-1998 (first entry)
 DE Amino acid sequence of a recombinant humanised antibody C4g1 heavy chain.
 KW Humanised antibody C4g1; heavy chain; humanised; immunoglobulin; Ig;
 KW mouse C4g1; antibody; inhibition; antigen; cardiovascular disease;
 KW thromboembolic disorder; cancer; acute myocardial infarction;
 KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;
 KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 PN US5777085-A.
 PD 07-JUL-1998.
 PF 17-MAY-1995; 458516.
 PR 03-MAY-1993; US-053159.
 PR 20-DEC-1991; US-812111.
 PR 09-JUN-1992; US-895952.
 PR 11-SEP-1992; US-944159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Co MS, Tso JY;
 DR WPI; 98-398136/34.
 PT New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4g1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
 PS Disclosure; Fig 7D; 35pp; English.
 CC This is the amino acid sequence of a fragment of a recombinant humanised antibody C4g1 heavy chain, used in the method of the invention involving the creation of a humanised immunoglobulin (Ig) derived from the mouse C4g1 antibody. The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute myocardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnosing

CC the presence and location of a thrombus, or certain types of cancer
 CC cells which develop GPIIb/IIIa on their surfaces, for the detection of
 CC GPIIb/IIIa antigens or for isolating platelets.
 SQ Sequence 235 AA;

Query Match 70.9%; Score 676; DB 1; Length 235;
 Best Local Similarity 82.8%; Pred. No. 8.5e-45;
 Matches 135; Conservative 6; Mismatches 16; Indels 6; Gaps 3;

OY 20 QVQLVQSGAEVKKPGASVKVSCKGSGYFTSYMMHWVRQAPQRLMEIGEDPSSENNY 79
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGIAFTNLIEMVRQAPQGLGVIYPSGGTNY 60
 OY 80 NQKFKGRVTLTVDISASTAYMELSLRSEDPAVYICAR--GGDGMWDYAIIDWGGTLYT 137
 DB 61 NEKFKGRVTLTVDESTNAYMELSLRSEDPAVYICARQDNY--GM---FAIWGGTLYT 116
 OY 138 VSSASTKGPVFPPLAPSSKSTSGTALGCLVKYDPEPTVS 180
 DB 117 VSSASTKGPVFPPLAPSSKSTSGTALGCLVKYDPEPTVS 159

RESULT 14

R28808 R28808 standard; Protein; 468 AA.

AC R28808:
 DT 02-APR-1993 (first entry)
 DE pre-5A8 humanised heavy chain.
 KW Vector: pMDR1002; NotI; HindIII; pMDR1001; PSAB132; PBAG101; E. coli;
 KW J4221(Iq); ampicillin; resistance; immunoglobulin; signal sequence;
 KW humanised; 5A8; heavy chain; variable; region; HV; IgG4; constant;
 KW HC; antibody; homolog; CD4; gp120; cell surface glycoprotein; CD4+;
 KW lymphocytes; helper; inducer; HIV; syncytia; formation.
 OS Synthetic.

FT Key Peptide Location/Qualifiers
 FT 1..19 /note="Immunoglobulin signal peptide"
 FT 20..141 /note="Humanised 5A8 HV"
 FT 142..468 /note="Human IgG4 HC"

FT region
 FT WO9209305-A.
 FN 11-JUN-1992.
 PD 27-NOV-1991; U08843.
 PR 27-NOV-1990; US-618542.
 PA (BROJ) BIOGEN INC.
 PI Burkiy LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
 DR N-PSDB: Q30910.
 PT New anti-CD4 antibody homologues - which bind CD4, do not block
 PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
 PT formation between CD4+ cells
 PS Disclosure: Page 135-56; 205pp; English.
 CC This sequence is encoded by the insert of the vector pMDR1002. Three
 CC fragments were used in the construction of pMDR1002; a 443 bp NotI/
 CC HindIII fragment of pMDR1001 (see Q30905), the 7913 bp NotI linearised
 CC pSAB132 (see Q30906), and a 2109 bp NotI/HindIII fragment of PBAG101
 CC (see Q30909). These fragments were ligated together and the ligation
 CC mixture was used to transform E. coli J4221(Iq) to ampicillin
 CC resistance. This sequence represents the immunoglobulin
 CC sequence, amino acids (AA) 1-122 of the humanised 5A8 heavy chain.
 CC variable region (HV) and AA114-AA478 of the human IgG4 heavy chain,
 CC ie, the constant region (HC). This polypeptide is an antibody homolog
 CC which was shown to bind to CD4 but did not block the binding of gp120
 CC to CD4. CD4 is a cell surface glycoprotein of CD4+ lymphocytes
 CC (helper/inducer cells). The homolog blocked HIV-induced syncytia
 CC formation. This homolog can be used in the detection, prophylaxis
 CC and treatment of diseases caused by infective agents whose primary
 CC targets are CD4+ cells.
 SQ Sequence 468 AA;

Query Match 70.3%; Score 670.5; DB 1; Length 468;
 Best Local Similarity 72.3%; Pred. No. 4.5e-44;
 Matches 133; Conservative 16; Mismatches 28; Indels 7; Gaps 2;

OY 1 MKCTVILFLVSTANVSQVQLVQSGAEVKKPGASVKVSCKGSGYFTSYMMHWVRQAP 60
 DB 1 KMTWVIFCLLVAPGASQVQLVQSGAEVKKPGASVKVSCKASGYTSTYIHVRQAP 60
 OY 61 GQLEWIGEDIPSESNINQKFKGRVTLTVDISASTAYMELSLRSEDPAVYICARGGY 120
 DB 61 GQLEWIGETIYPNGTGYDEKFKKATVITDPSNTAYMELSLRSEDPAVYICAR--- 118
 OY 121 DGMWDA---IDYWGQGLTVTVSSASTKGPVFPPLAPSSKSTSGTALGCLVKYDPEP 176
 DB 118 EKDNVATGAMPAYWQGLTVTVSSASTKGPVFPPLAPSSKSTSGTALGCLVKYDPEP 177
 OY 177 TVVS 180
 DB 178 TVVS 181

RESULT 15

W14941 W14941 standard; Protein; 464 AA.

AC W14941:
 DT 16-JUN-1997 (first entry)
 DE 3F4 Human IgG4 expression plasmid insert product (heavy chain).
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 OS Mus sp.

PN WO97111971-A1.
 PD 03-APR-1997.
 PT 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Mattis LA, Mueller EE, Mueller JP, Rollins S;
 PI Roher RP.
 DR WPI: 97-212855/19.
 DR N-PSDB: T62938.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure: Page 62-64; 105pp; English.
 CC Heavy chain (W14941) and light chain (W14942) sequences
 CC correspond to murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 3F4 (see also W14937-38). They
 CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
 CC also T62938). A chimeric antibody specific for porcine VCAM can be
 CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 SQ Sequence 464 AA;

Query Match 70.2%; Score 669.5; DB 1; Length 464;
 Best Local Similarity 70.5%; Pred. No. 5.3e-44;
 Matches 129; Conservative 17; Mismatches 28; Indels 9; Gaps 2;

OY 1 MKCTVILFLVSTANVSQVQLVQSGAEVKKPGASVKVSCKGSGYFTSYMMHWVRQAP 60
 DB 1 KMTWVILFLVSTAGVSVQVQSGAEVKKPGASVSLSCASGYTNSTWQVQKORP 60
 OY 61 GQLEWIGEDIPSESNINQKFKGRVTLTVDISASTAYMELSLRSEDPAVYICAR--- 118
 DB 61 GQLEWIGETIYPNGDGYTQKFKKATVITDKSSTAYMELSLSDSDAVYICARTV 120
 OY 118 GGYDGMWDAIDYWGQGLTVTVSSASTKGPVFPPLAPSSKSTSGTALGCLVKYDPEP 177
 DB 121 GGY-----FDYWGQGLTVTVSSASTKGPVFPPLAPSSKSTSGTALGCLVKYDPEP 174

Tue May 11 13:50:11 1999

us-08-700-737-19.rag

Page 8

Oy 178 rvs 180
111
Db 175 rvs 177

Search completed: May 11, 1999, 12:14:57
Job time: 2104 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 12:00:33 ; Search time 962.98 Seconds

(without alignments)
1534.328 Million cell updates/sec

Title: US-08-700-737-20

Perfect score: 413
Sequence: 1 ATGAAGTTCCTGTTAGGCT.....AAACGGCGCTGATCGCGGCC 413

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database: GenBank1.*

1: gb_ba1.*
2: gb_ba2.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_p11.*
9: gb_p12.*
10: gb_p13.*
11: gb_p14.*
12: gb_p15.*
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34: gb_p37.*
35: gb_p38.*
36: gb_p39.*
37: gb_p40.*
38: gb_p41.*
39: gb_p42.*
40: gb_p43.*
41: gb_p44.*
42: gb_p45.*
43: gb_p46.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	340	82.3	396	13	MMU16688	U16688 Mus musculus
2	327.2	79.2	396	13	MUSIGKBN	M15874 Mouse Ig ac
3	312.2	75.6	417	13	MMU62051	U62051 Mus musculus
4	308.8	74.8	538	13	MMIGVK	X00045 Mouse mRNA
5	308.2	74.6	538	13	MUSIGKAT	K00709 Mouse Ig ka
6	305.8	74.0	456	13	MMU39901	U39901 Mus musculus
7	302.6	73.3	436	13	MMU012556	AJ012556 Mus muscu
8	300.2	72.7	432	13	MMU62054	AJ01812 Mus muscu
9	299.4	72.5	432	13	MMU62054	U62054 Mus musculus
10	299	72.4	339	13	MUSIGKCOL	M24275 Mouse Ig ge
11	297.2	72.0	404	13	RAFIGCD2L	M87786 Rat (hybrid
12	294.6	71.3	956	13	MMKAPL1	X87231 M.musculus
13	294.6	71.3	421	13	MMY17589	Y17589 Mus musculus
14	294.2	71.2	805	13	MUSIGKIDH	L12156 W3129; Mus
15	293.6	71.1	416	13	MUSIGKICL	M20828 Mouse IgG2a
16	292	70.7	426	13	MUSIGVK	M55313 Mouse Igr p
17	291.4	70.6	394	6	AR022601	AR022601 Sequence
18	289.2	70.0	351	13	MMU22804	U22804 Mus musculus
19	288.8	69.9	393	13	AF045491	AF045491 Mus muscu
20	288.2	69.8	420	13	S82491	S82491 Tg10 kappa-
21	288.2	69.8	957	13	MMU65535	U65535 Mus musculus
22	288	69.7	336	13	MMIGG2AK	X74588 M.musculus
23	287.2	69.5	393	13	MUSIGK313A	L38105 Mus musculus
24	286.6	69.4	394	6	AR022585	AR022585 Sequence
25	286.6	69.4	394	13	S67233	S67233 Igg3VL-muc1
26	286.2	69.3	339	13	MUSIGKCOI	M24272 Mouse Ig ge
27	286.2	69.3	339	13	MUSIGKCOK	M24274 Mouse Ig ge
28	286.2	69.3	323	13	MUSIGKAPD	M64152 Mus musculus
29	286.2	69.3	323	13	MUSIGKAPM	M64161 Mus musculus
30	286	69.2	427	6	A25561	A25561 H.sapiens B
31	286	69.2	427	6	I26967	I26967 Sequence 8
32	285.6	69.2	393	13	AF013576	AF013576 Mus muscu
33	285.6	69.2	393	13	MUSIGK24A	M32382 Mus musculus
34	284	68.8	434	6	A25576	A25576 M.musculus
35	284	68.8	434	6	I26965	I26965 Sequence 4
36	284	68.8	393	13	MUSIGK514	L39088 Mus musculus
37	284	68.8	393	13	MUSIGK940A	L39104 Mus musculus
38	284	68.8	393	13	MUSIGK1240	M32384 Mus musculus
39	283.4	68.6	394	6	AR022571	AR022571 Sequence
40	282.4	68.4	393	13	AF045490	AF045490 Mus muscu
41	282.4	68.4	393	13	MUSIGK1025	M32381 Mus musculus
42	281.2	68.1	384	6	AR013851	AR013851 Sequence
43	280.8	68.0	393	13	AF045494	AF045494 Mus muscu
44	280.8	68.0	393	13	MUSIGK4420	L39087 Mus musculus
45	280.8	68.0	420	13	MMLB41LEV	X65775 M.musculus

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL
1	MMU16688	Mus musculus Ig light chain leader and variable region Vx II gene family mRNA, partial cds.	U16688	91041798	house mouse.	Mus musculus	Eukaryotae; mitochondria; eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 396)	White,K.D., Frank,M.B., Foundling,S. and Waxman,F.J.	Effect of immunoglobulin variable region structure on C3b and C4b deposition	Mol. Immunol. 33 (9), 759-768 (1996)	96406984	2 (bases 1 to 396)	Frank,B.	Direct Submission	Submitted (27-OCT-1994) Bart Frank, Arthritis and Immunology

ACCESSION	U62051
NTID	g1438582
KEYWORDS	
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 417)
TITLE	Diaz, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P.M. and Dighiero, G.
JOURNAL	Structural and affinity studies of IgM polyclonal natural autoantibodies
MEDLINE	J. Immunol. 158 (2), 968-976 (1997)
REFERENCE	2 (bases 1 to 417)
AUTHORS	Diaz, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P.M. and Dighiero, G.
TITLE	Direct Submission
JOURNAL	Submitted (25-JUN-1996) Laboratoire d'Immunohematologie et d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris 75724 Paris Cedex 15, France
FEATURES	Location/Qualifiers
source	1..417
	/organism="Mus musculus"
	/strain="NZB"
	/note="hybridoma A9A7; 6-day-old spleen cells fused with X63.653 line"
	/db_xref="taxon:10090"
	<1..>417
	/codon_start=1
	/product="polyreactive autoantibody, immunoglobulin light chain"
CDS	/db_xref="PID:g1438583"
	/translation="MKLPRLVLLFWIPASSSDVMYOTPLSPVSLGQASISCRSSQSLSNSGNLTLYWLOKPOSPRLILRYVSNFSGVPDPFSGSSTDFTLISRYSFAEIDLGYVCFEGCHVPEFTFGSSGRLETRADAAPTV"
BASE COUNT	97 a 99 c 105 g 116 t
ORIGIN	
Query Match	75.6%; Score 312.2; DB 13; Length 417;
Best Local Similarity	86.4%; Pred. No. 6.1e-93;
Matches 357; Conservative	0; Mismatches 53; Indels 3; Gaps 1;
Oy	1 ATGAAGTGGCCGTAGAGCTGTGTGGTCCTGTTGTTCTGCATTCCTGTTCCGAGGT 60
Db	1 ATGAAGTGGCCGTAGAGCTGTGTGGTG---CCTGTTCTGCATTCCTGTTCCGAGCA 57
Oy	61 GATGTTGATGACTCAAAGTCCACTCTGCCCTGTCACCCTGGAGAACACTTCT 120
Db	58 GATGTTGATGATCACCAAACTCCACTCTCCCGCTGTCAAGTCTGGAGATCAAGTTCC 117
Oy	121 ATCTTGTGAGGTCTAGTTCAGAGCTCTTGCACAAGATTATGGAGAACACTATTGTTGG 180
Db	118 ATCTTGTGAGATCTAGTTCAGAGCTCTTGTACACACAAGAATAAGAACACTATTATATGG 177
Oy	181 TACCTGAGAAAGCCCTGGCCAGTCTCCACAGCTCCCTCATCTATAGGATTTCCAAGATT 240
Db	178 TACCTGAGAAAGCCAGGCCAGTCTCCAAAGCTCCCTGATCTTAAGGATTTCCAAGCAATT 237
Oy	241 TCTGGGGTCCAGACAGTTCAAGTGGAGTGTAGGAGCAAGATTTCACATCAAGATC 300
Db	238 TCTGGGGTCCAGACAGTTCAAGTGGAGTGTAGGAGCAAGATTTCACATCAAGATC 297
Oy	301 TCAGCATGAGAGCTGAGGACGTTGGAGTGTACTGCTTACAAGATACATCAGCCG 360
Db	298 ACACAGATGAGAGCTGAGGATCTGGGAGTTTATCTGCTTCAAGATACATCTTCTCT 357
Oy	361 TACAGTTTCGAGCAGAGGACCAAGATGGAATAAAGAGGCGTAGTGGCGGC 413
Db	358 TTCAGTTTCGAGTGGGAGCAAGATTTGGAATAAAGAGGCGTAGTGGCTGACCC 410:

LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE
MMIGVK	Mouse mRNA for anti-GAT antibody. (poly Glu-60 Ala-30 Tyr-10 random terpolymer).	X00045 K00709	952532	Ig kappa light chain; immunoglobulin; signal peptide.	ORGANISM
REFERENCE	1 (bases 1 to 538)				
AUTHORS	Schiff,C., Corbet,S., Millil,M. and Fougereau,M.				
TITLE	Interstrand conservation of the murine GAT-specific antibody V kappa repertoire as analyzed at the germline gene level				
JOURNAL	EMBO J. 2 (10), 1771-1776 (1983)				
MEDLINE	84057697				
COMMENT	Data kindly reviewed (09-MAY-1985) by M. Fougereau.				
FEATURES	location/Qualifiers				
Source	1..538				
ORIGIN	/organism="Mus musculus"				
ORIGIN	/db_xref="taxon:10090"				
ORIGIN	1..>538				
ORIGIN	/note="messenger RNA"				
ORIGIN	132..188				
ORIGIN	/note="signal peptide"				
ORIGIN	132..>538				
ORIGIN	/note="variable region joining segment (538 is 2nd base in codon)"				
ORIGIN	132..>538				
ORIGIN	/note="variable region joining segment (538 is 2nd base in codon)"				
ORIGIN	/codon_start=1				
ORIGIN	/db_xref="PID:g52533"				
ORIGIN	/translation="MKPLRVLLVLMFVIPASXSDVYVNTOTPLSPVSLGDOASICRS				
ORIGIN	SOSIVSNGNTLYWYKROGOSKILLITYVSNRFSVPDRFSGSSGDTFLINISRV				
ORIGIN	EAEIMCYVCFOGCIHYPHTGGGKLEIKADAA"				
ORIGIN	BASE COUNT 127 a 133 c 132 g 143 t 3 others				
ORIGIN	Query Match 74.8% Score 308.8; DB 13; Length 538;				
ORIGIN	Best Local Similarity 86.1% Pred. No. 8.5e-92;				
ORIGIN	Matches 353; Conservative 0; Mismatches 54; Indels 3; Gaps 1;				
ORIGIN	1 ATGAAGTGCCTGTAGGCTGTGGCTGTGCTCTGTGTCTGTGATGATCTGTTCCGAGAGT 60				
ORIGIN	132 ATGAAGTGCCTGTAGGCTGTGGCTGTGCTCTGTGTCTGTGATGATCTGTTCCGAGAGT 188				
ORIGIN	61 GATGTGTGATGACTCAAAAGTCCACTCTCCCTGCTGACCCCTGGAGAACAGCTTCT 120				
ORIGIN	189 GATGTGTGATGACCCCAACATCCACTCCCTGCTGACCCCTGGAGAACAGCTTCT 248				
ORIGIN	121 ATCTCTTCAGAGCTTCAGTACAGAGCTTTCACAAAGATTGAGGAACACCTATTGCTTG 180				
ORIGIN	249 ATCTCTTCAGATATCTAGTACAGACATTGTATACAGTAATGAAACACCTATTATTATGG 308				
ORIGIN	181 TACCTGAGAAAGCTGGCCAGCTCTCCACAGCTCTCATCTATGAGATTTCACAGAGATT 240				
ORIGIN	309 TACCTGAGAAACAGAGCCAGCTCTCCAAAGCTCTGATCTACAGGGTTTCCACCGAATT 368				
ORIGIN	241 TCTGGGGCCACAGACAGTTTCAGTGGCAGTGGTTCAGGGACAGATTTCACACTCAAGATC 300				
ORIGIN	369 TCTGGGGCCACAGACAGTTTCAGTGGCAGTGGTTCAGGGACAGATTTCACACTCAAGATC 428				
ORIGIN	301 TCGGAGTAGAGAGCTGAGAGAGTGGAGATGATTAAGTCTTACAAAGAGACATCAGCGG 360				
ORIGIN	429 AGCAGAGTAGAGAGCTGAGAGATGATTAAGTCTTACAAAGAGACATCAGTTCTT 488				
ORIGIN	361 TACACGTTTCGACACAGGGGACCAAGGTGGAATTAACGGGCTGATGGCGC 410				

DB	489	CACACGTTTCGAGGGGGGACCAAGCTGGAATAAAGGGCTGATGCTGC	538
RESULT	5		
MUSIGRAT		538 bp	RNA
LOCUS			ROD
DEFINITION			01-MAY-1984
ACCESSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
FEATURES			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
1			
132			
61			
169			
121			
249			
181			
309			
241			
369			
301			
429			
361			
489			
RESULT	6		
MUSJ9901			
LOCUS			
DEFINITION			
ACCESSION			
NID			

KEYWORDS	house mouse.
SOURCE	Mus musculus
ORGANISM	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 456)	Schoppel, K., Hassfurter, E., Britz, W., Ohlin, M., Borrebaeck, C.A. and Mach, M.
TITLE	Antibodies specific for the antigenic domain 1 of glycoprotein B (gpUL5) of human cytomegalovirus bind to different substructures
JOURNAL	Virology 216 (1), 133-145 (1996)
MEDLINE	96187797
REFERENCE 2 (bases 1 to 456)	Schoppel, K.
AUTHORS	Direct Submission
TITLE	Submitted (02-NOV-1995) Michael Mach, Institute of Virology, University Erlangen-Nuernberg, Schlossgarten 4., 91054 Erlangen, Germany
FEATURES	Location/Qualifiers
source	1..456
	/organism="Mus musculus"
	/strain="Balb/C"
	/note="monoclonal antibody 7-17"
	/db_xref="taxon:10090"
CDS	1..>456
	/codon_start=1
	/product="anti-glycoprotein-B of human Cytomegalovirus immunoglobulin VI chain"
	/db_xref="PID:g1680671"
	/translation="MKLPRLVLMFNPASSDPVVMQPLSPVSLGGASISCRSOSVSHSSGNTLEWYDQKPEQSKLIRVSNFSGVPDFFSSGSDTLTISRFAEDELGYVCFQSGSHVPTFESGRLIKRADAAPIVASIFPPSKLIDDK"
BASE COUNT	110 a 109 c 113 g 124 t
ORIGIN	
Query Match	74.0%; Score 305.8; DB 13; Length 456;
Best Local Similarity	85.5%; Pred. No. 8.1e-91;
Matches 353; Conservative	0; Mismatches 57; Indels 3; Gaps 1;
Oy	1 ATGAAGTGGCCGTAGAGCTGTGTGCTCTGTTCTGTGGATTCGTTCCGGAGGT 60
Db	1 ATGAAGTGGCCGTAGAGCTGTGTGCTCTGTTCTGTGGATTCGTTCCGGAGGT 57
Oy	61 GATGTTGTGATGACTCAAAAGTCCACTCTCCCTGCTACCCCTGGAGAACCACTTCT 120
Db	58 GATGTTGTGATGATCAAAAGTCCACTCTCCCTGCTACCCCTGGAGAGTCAACCTTCC 117
Oy	121 ATTCCTTCAGCTCAGTACAGAGCTTCCAAAGATTAATGGGAACACCTATTGTCCTGG 180
Db	118 ATTCCTTCAGCTCAGTACAGAGCTTTCATCTATGATGGAACACCTATTAGAAATGG 177
Oy	181 TACCTGCAGAAAGCCCTGGCCAGCTCTCCACAGCTCCATCTATGGGATTTCCAAAGATT 240
Db	178 TACCTGCAGAAAGCCAGGCGCAGTCTCCAAAGCTCCGATCTACAGAGTTTCCAAAGATT 237
Oy	241 TCTGGGGTCCACAGACAGTTCACTGTGCACTGTGTAGGACAGATTTCAACTCAAGATC 300
Db	238 TCTGGGGTCCACAGACAGTTCACTGTGCACTGTGTAGGACAGATTTCAACTCAAGATC 297
Oy	301 TCGCAGTAGAGAGCTGAGAGAGCTGGGAGATGTATTCCTCTTCAAGTAGTACATCAGCG 360
Db	298 AGCAGAGTAGAGAGCTGAGAGATCTGGGAGATTTATTACTGCTTTCAAGGTTACATGTTCCG 357
Oy	361 TACACGTTTCGAGACAGGAGACCAAGGTGGAATTAATAAGGGGCTGATCGCGGCC 413
Db	358 TATACGTTTCGAGATCGGGACCAAGCTGGAATTAATAAGGGGCTGATCGTGCACC 410

DEFINITION Mus musculus mRNA for H3 specific immunoglobulin, kappa chain,
variable region, partial.
ACCESSION AJ012556
NID 93860516
KEYWORDS immunoglobulin superfamily; kappa chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 436)
Wigley, N.G., Brown, E.B., Daniels, R.S., Douglas, A.R., Skehel, J.J.
and Wiley, D.C.
TITLE Electron microscopy of influenza haemagglutinin-monovalent antibody
complexes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 436)
AUTHORS Daniels, R.S.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1998) Daniels R.S., Virology Division, National
Institute for Medical Research, The Ridgeway, Mill Hill, London,
NW7 1AA, UK
FEATURES
source 1..436
location/Qualifiers
source 1..436
/organism="Mus musculus"
/db_xref="taxon:10090"
1..432
/organism="Mus musculus"
/db_xref="taxon:10090"
/rearranged
/cell_type="hybridoma"
/product="immunoglobulin, kappa chain, variable region"
/note="monoclonal antibody, Hc45; specific for influenza
haemagglutinin H3"
/codon_start=1
/product="immunoglobulin, kappa chain, variable region"
/db_xref="PID:e1341342"
/db_xref="PID:g3860517"
/translation="MKLPVRLVLMFMIPASSDVMTQPLSPVSIADQASISCRS
SOTVHNGNTVLMHLYKRGOSPKLLIVKSNRFGVDPDRFGSGSGIDFTIKIRIV
EADLDGVYICSONTHVPTFGGSKLEIKRADAPVSIFFPS"
BASE COUNT 107 a 114 c 101 g 114 t
ORIGIN
Query Match 73.3%; Score 302.6; DB 13; Length 436;
Best Local Similarity 85.0%; Pred. No. 9.3e-90;
Matches 351; Conservative 0; Mismatches 59; Indels 3; Gaps 1;
QY 1 ATGAAGTGGCTGTAGGCTGTGCTCTGTTGTTGATTCCTGTTCCGGAGGT 60
Db 1 ATGAAGTGGCTGTAGGCTGTGCTCTGTTGTTGATTCCTGTTCCGGAGGT 57
QY 61 GATGTTGTGATGACTCAAGTCACTCTCCCTGCTGACCCCTGGAGAACGCTTCT 120
Db 58 GATGTTGTGATGACTCAAGTCACTCTCCCTGCTGACCCCTGGAGAACGCTTCT 117
QY 121 ATCTCTGAGGCTTATCAGAGTCTTGCAAGAGTTATGGAACACCTATTGTTCTGG 180
Db 118 ATCTCTGAGGCTTATCAGAGTCTTGCAAGAGTTATGGAACACCTATTGTTCTGG 177
QY 181 TACCTGAGAGGCTGCGAGTCTCCACAGTCTCTCATCTATGGAGTTTCCACAGATT 240
Db 178 TACCTGAGAGGCTGCGAGTCTCCACAGTCTCTCATCTATGGAGTTTCCACAGATT 237
QY 241 TCTGGGGTCCAGACAGGTTCAAGTGGAGTGGTTCAGGAGACAGATTTCACACTCAGATC 300
Db 238 TCTGGGGTCCAGACAGGTTCAAGTGGAGTGGTTCAGGAGACAGATTTCACACTCAGATC 297
QY 301 TCGGAGTAAAGGCTGAGGAGTGGAGTGTATATGCTTACAAAGTACACATCAGCCG 360
Db 298 AGCAGAGTGAAGGCTGAGGAGTGGAGTGTATATGCTTCTCAAAATACACATGTTCCG 357

QY 361 TACACGTTCCGACAGGGGACCAAGTGGAAATAAAACGGGCTGATGGCGCC 413
Db 358 TACACGTTCCGACAGGGGACCAAGTGGAAATAAAACGGGCTGATGGCGCC 410
RESULT 8
HS001812 387 bp mRNA ROD 30-MAR-1998
LOCUS Mus musculus partial mRNA sequence for immunoglobulin light chain
DEFINITION V-region (clone 2C7/K18F).
ACCESSION AJ001812
NID 93004453
KEYWORDS immunoglobulin; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 387)
McElveen, J., Clark, M.R., Smith, S.J., Sewell, H.F., and Shakh, F.
TITLE Primary sequence and molecular model of the variable region of a
mouse monoclonal anti-Der P I antibody showing the same epitope
specificity as human IgE: Production of a mouse monoclonal
anti-Idiotypic that recognises a cross-reactive idiotype on human
IgE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 387)
AUTHORS Clark, M.R.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-1997) Clark M.R., Pathology Department,
University of Cambridge, Tennis Court Road, Cambridge, CB2 1QP, UK
FEATURES
source 1..387
location/Qualifiers
source 1..387
/organism="Mus musculus"
/strain="BAJB/c"
/db_xref="taxon:10090"
/rearranged
/cell_line="2C7"
/cell_type="hybridoma"
/clone="2C7/K18F"
/tissue_type="B-cell hybridoma"
/note=">387
/codon_start=1
/evidence="experimental
/product="variable region of IgE light chain"
/db_xref="PID:e1284813"
/db_xref="PID:g3004454"
/translation="DVLMTQPLSLPVSPGQVSISSRSQSLANSYNTLYSLYHK
PGSPQLIVGISDRFSGVDPDRFGSGSGTDTLTKSTIKPEDLGWYCLDGTQHPWT
FGGSKLEIKRADAPVSIFFPSSEQ"
BASE COUNT 96 a 100 c 91 g 100 t
ORIGIN
Query Match 72.7%; Score 300.2; DB 13; Length 387;
Best Local Similarity 90.7%; Pred. No. 5.7e-89;
Matches 330; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 61 GATGTTGTGATGACTCAAGTCACTCTCCCTGCTGACCCCTGGAGAACGCTTCT 120
Db 1 GATGTTGTGATGACTCAAGTCACTCTCCCTGCTGACCCCTGGAGAACGCTTCT 60
QY 121 ATCTCTGAGGCTTATCAGAGTCTTGCAAGAGTTATGGAACACCTATTGTTCTGG 180
Db 118 ATCTCTGAGGCTTATCAGAGTCTTGCAAGAGTTATGGAACACCTATTGTTCTGG 120
QY 181 TACCTGAGAGGCTGCGAGTCTCCACAGTCTCTCATCTATGGAGTTTCCACAGATT 240
Db 61 ATCTCTGAGGCTTATCAGAGTCTTGCAAGAGTTATGGAACACCTATTGTTCTGG 120
QY 241 TCTGGGGTCCAGACAGGTTCAAGTGGAGTGGTTCAGGAGACAGATTTCACACTCAGATC 300
Db 121 TCTGGGGTCCAGACAGGTTCAAGTGGAGTGGTTCAGGAGACAGATTTCACACTCAGATC 180
QY 241 TCTGGGGTCCAGACAGGTTCAAGTGGAGTGGTTCAGGAGACAGATTTCACACTCAGATC 300
Db 181 TCTGGGGTCCAGACAGGTTCAAGTGGAGTGGTTCAGGAGACAGATTTCACACTCAGATC 240

QY	301	TCGCAGTAGAGCGCTGAGGACCTGGGAGCTGTCTACTGCTTACAGTACATCAGCG	360
DB	241	AGCACATTAACACCTGAGAGACTGGGAATGTTACTGCTTTCAAGGTACACATAGCG	300
QY	361	TACACGTTGCGACAGGAGGACCAAGGTGGAATAAAGGGCGTATGCGGCGC	413
DB	301	TGGAGCTTCGGGTGAGGACCAAGCTGGAAATCAACAGGCGTGATGCTGACCC	353
RESULT 9			
	MM062054	432 bp	ROD
	LOCUS		19-FEB-1997
	DEFINITION	Mus musculus polyreactive autoantibody, immunoglobulin light chain kappa mRNA, partial cds.	
	ACCESSION	U62054	
	KEYWORDS	g1438588	
	SOURCE	house mouse.	
	ORGANISM	Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 432)	Diaw, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P. M. and Dighiero, G.	
AUTHORS	structural and affinity studies of IgM polyreactive natural autoantibodies		
TITLE	J. Immunol. 158 (2), 968-976 (1997)		
JOURNAL	97146071		
MEDLINE	2 (bases 1 to 432)		
REFERENCE	Diaw, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P. M. and Dighiero, G.		
AUTHORS	Direct Submission		
TITLE	Submitted (25-JUN-1996) Laboratoire d'Immunohematologie et d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris 75724 Paris Cedex 15, France		
JOURNAL	Location/Qualifiers		
FEATURES	1..432		
SOURCE	/organism="Mus musculus"		
	/strain="BALB/c"		
	/note="Hybridoma F9A7; adult in vivo spleen cells stimulated with IFS, fused with X63.653 line"		
	/db_xref="taxon:10090"		
	16..>432		
	/codon_start=1		
	/product="polyreactive autoantibody, immunoglobulin light chain kappa"		
	/db_xref="PID:g1438589"		
	/translation="MKLPKRLVLMFWIPASSDVLMTQPLSLPVLGDAISCRSSQSIVHSNGNTLWYLOKPGQSPKRLIKVSNFSGVPPRFSGSGSGIDFTLKISRYEAEDLGYVCFQSGSHVPEFSGSKLEIKRADAPTV"		
BASE COUNT	109 a	100 c	106 g
ORIGIN	117 t		
Query Match	72.5%;	Score 299.4;	DB 13; Length 432;
Best Local Similarity	84.5%;	Pred. No. 1.1e-88;	
Matches 349; Conservative	0;	Mismatches 61;	Indels 3; Gaps 1;
QY	1	ATGAAGTGGCCCTGTAGAGCTGTGGTGCCTCTGCTGTCTGTGGATTCCTGTTCCGGAAGT	60
DB	16	ATGAAGTGGCCCTGTAGAGCTGTGGTGCCTCTGATGTTCTGTGATTCCTGCTTCAGCAGT	72
QY	61	GATGTTGATGATCAACAAGTCCATCTCCCGCTGCACCCCTGGAGAACCACTCT	120
DB	73	GATGTTGATGATCAACAAGTCCATCTCCCGCTGCACCTTGGAGATCAAGCTCC	132
QY	121	ATCTTTGACAGCTAGTCAGAGTCTTGCACAAAGATTATGGACACCTATTGTCTTG	180
DB	133	ATCTTTGACAGCTAGTCAGAGTCTTGCACAAAGATTATGGACACCTATTGTGATG	192
QY	181	TACGCGAAGACCTGGCGCACTGCTCCACAGCTCCATCTATATGGATTTCCACAGATTT	240

Db	193	TACCTGTCAGAAACACGGCCAGCTCTCCAAAGCTCCCTGATCTACAAAGTTTCCACAGGATTT	252
Qy	241	TCGTGGGGTCCACAGACAGGTTCACTAGTGGCAGTGGTTCCAGGACAGATTTCCACTCAAGATC	300
Db	253	TCGTGGGGTCCACAGACAGGTTCACTAGTGGCAGTGGTTCCAGGACAGATTTCCACTCAAGATC	312
Qy	301	TCGCAGTAGAGGCGTAGAGACGTGGGAGTGTATTTCTCTTACGATTAACAGTAGACATCAGACG	360
Db	313	ACCAAGATGTGAGGCTGAGGATCTGGGAGTGTATTTACTCTTTCACAGGTTCAACATGTTCCA	372
Qy	361	TACAGCTTCGACAGAGGACCAAGGTGGAATAAACAAGGCGTATCGCGGCC	413
Db	373	TTACAGTTCGGCTCGGGGACAAAGTTGGAAATAAACAAGGCGTATCGCGGCC	425
RESULT	10		
MUSICCOL			
LOCUS	MUSIGRCOL	339 bp	mRNA
DEFINITION	Mouse Ig germ-line Q52 kappa-chain mRNA (V-J2), partial cds.		
ACCESSION	M24275		
KEYWORDS	9137085		
SOURCE	C-region; J-region; germ-line; immunoglobulin light chain; immunoglobulin-kappa variable region; processed gene.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryotes: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorphae; Muridae; Mus.		
AUTHORS	1 (bases 1 to 339)		
TITLE	Matsuda, T. and Kabat, E. A.		
JOURNAL	Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1---6)dextran		
MEDLINE	J. Immunol. 142 (3), 863-870 (1989)		
FEATURES	89110062		
source	Location/Qualifiers		
	1..339		
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	/db_xref="taxon:10090"		
	/clone="36.1.2D"		
	<1..>339		
	/note="Ig kappa-chain (V-J2)"		
	/codon_start=1		
	/db_xref="PID:g197086"		
	/translation="DYVVTQPLSLPVSFQGVDSISCRSSGLANSYGNVYLSWYLRKPGSPOLIIYGISKRFSGVDPFRFSGSGSDFTLKISTIKRPEDIGMYCICLQSTHQPPTYFGGSKLEIKR"		
CDS			
BASE COUNT	87 a	80 c	84 g
ORIGIN			88 t
Query Match	72.4%; Score 299; DB 13; Length 339;		
Best Local Similarity	92.6%; Pred. No. 1.4e-88;		
Matches 314; Conservative	0; Mismatches 25; Indels 0; Gaps 0;		
Qy	61	GATGTTGTGATGACTCAAAAGTCCACTTCCTCCCTGCTCACCCCTGGAAACAGCTTCT	120
Db	1	GATGTTGTGATGACTCAAAAGTCCACTTCCTCCCTGCTCACCCCTGGAAACAGCTTCT	60
Qy	121	ATCTCTGACAGTCTAGTCAGAGTCTTTCGAAAGATATATGGAAACACTATTTGCTCTGG	180
Db	61	ATCTCTGACAGTCTAGTCAGAGTCTTTCGAAACAGATATATGGAAACACTATTTGCTCTGG	120
Qy	181	TACCTGACAGAACCTCGGCGACGTCCTACAGAGCCCTCATCTATATGGATTTCCACAGATTT	240
Db	121	TACCTGACAGAACCTCGGCGACGTCCTACAGAGCTCTCATCTATATGGATTTCCACAGATTT	180
Qy	241	TCGTGGGGTCCACAGACAGGTTCACTAGTGGCAGTGGTTCCAGGACAGATTTCCACTCAAGATC	300
Db	181	TCGTGGGGTCCACAGACAGGTTCACTAGTGGCAGTGGTTCCAGGACAGATTTCCACTCAAGATC	240
Qy	301	TCGCAGTAGAGGCGTAGAGACGTGGGAGTGTATTTCTCTTACGATTAACAGTAGACATCAGACG	360

Query Match	Best Local Similarity	Score	DB	Length
Matches 320: Conservative	0: Mismatches	43: Indels	0: Gaps	0
71.2%	88.2%	Pred. No. 6.2e-87;		
294.2	DB 13;	Length 805;		
gene	/gene="Irg"	/Label=leader	1..466	
misc_signal	/gene="Irg"	48..55		
intron	/gene="Irg"	/note="putative splice donor sequence"	50..455	
misc_feature	/gene="Irg"	145..146		
misc_feature	/gene="Irg"	/note="cryptic splice acceptor site in cell line 5S"	152..153	
misc_feature	/gene="Irg"	/note="deletion breakpoint site in cell line 5S"	275..276	
misc_feature	/gene="Irg"	/note="cryptic splice acceptor in cell line R15"	294..313	
misc_feature	/gene="Irg"	/note="deleted in cell line R15"	/citation=[3]	
misc_signal	/gene="Irg"	436..455		
exon	/gene="Irg"	/note="putative splice acceptor sequence"	467..805	
gene	/gene="Irg"	/Label=Kappa	467..805	
misc_feature	/gene="Irg"	/note="immunoglobulin kappa variable region"	537..538	
misc_feature	/gene="Irg"	/note="immunoglobulin kappa variable region"	537..538	
misc_feature	/gene="Irg"	/note="cryptic splice acceptor site, used in cell lines R15, 5S"	/citation=[1]	
misc_feature	/gene="Irg"	/note="sequences deleted in cell line 5S"	/citation=[2]	
misc_feature	/gene="Irg"	/note="immunoglobulin kappa variable region"	628..781	
misc_feature	/gene="Irg"	/note="sequences deleted in cell line 5S"	/citation=[2]	
BASE COUNT	220 a	158 c	185 g	242 t
ORIGIN				

DB	743	TCGTTACAAAGGTTACATCAGACCGCTCCGCTTCGCTGCTGGAGACCAAGCTGAGCTGAAA	802
QY	397	CGG 399	
DB	803	CGG 805	
RESULT	15		
MUSIGKCL			
LOCUS	MUSIGKCL	416 bp	ROD
DEFINITION	Mouse IgG2ak rearranged kappa light-chain mRNA		15-MAR-1989
ACCESSION	(V-J-kappa) anti-DNA autoantibody.		
KEYWORDS	M20828		
SOURCE	V-region; autoantibody; immunoglobulin kappa-chain; immunoglobulin light chain; immunoglobulin-kappa.		
ORGANISM	Mouse (strain MRL/Mp -1pr/1pr) spleen hybridoma cell line MRL-DNA4, cDNA to mRNA.		
REFERENCE	Mus musculus		
AUTHORS	Eukaryotes: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 416)		
JOURNAL	Kofler, R., Strohal, R., Balderas, R.S., Johnson, M.E., Noonan, D.J., Duchosal, M.A., Dixon, F.J. and Theofilopoulos, A.N.		
MEDLINE	Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice		
COMMENT	J. Clin. Invest. 82, 852-860 (1988)		
FEATURES	Drift entry and computer-readable sequence [1] kindly submitted by R. Kofler 28-JUL-1988.		
source	Location/Qualifiers		
MRNA	1..416		
	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
	1..>416		
	/note="IgG2ak mRNA"		
s1g_peptide	24..80		
	/note="Ig light chain signal peptide"		
CDS	24..>416		
	/note="IgG2ak light chain precursor"		
	/codon_start=1		
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	EAEDLVYPCGQSTHVPRTSSKRLKIK"		
	81..>416		
mat_peptide	/note="Ig light chain"		
BASE COUNT	101 a 102 c 99 g 114 t		
ORIGIN	Chromosome 6.		
Query Match	71.1%; Score 293.6; DB 13; Length 416;		
Best Local Similarity	85.6%; Pred. No. 8.8e-87;		
Matches 339; Conservative	0; Mismatches 54; Indels 3; Gaps 1;		
QY	1	ATGAGTGGCCGTGATGAGCTGTGCTGCTCTGTTCTGATTCCTGTTCCGGAGGT	60
DB	24	ATGAAGGTGCGCTGATGAGCTGTGCTGCTGATTCCTGTTCCGGAGGT	80
QY	61	GATGTTGATGATCAAGTCCATCTCCCTGCTGACCCCTGGAGAACAGCTCT	120
DB	81	GATGTTGATGATCAAGTCCATCTCCCTGCTGACCCCTGGAGAACAGCTCT	140
QY	121	ATCTCTTCAGGCTAGTTCAGAGTCTTGCACCAAGTATGGGACACCTATTGCTTGG	180
DB	141	ATCTCTTCAGAGTTCAGAGTCTTGCACCAAGTATGGGACACCTATTGCTTGG	200
QY	181	TACCTGCAGAAAGCCCTGGCCAGTCTCCACAGTCCCTCATCTATGGATTTCCACAGATT	240
DB	201	TACCTGCAGAAAGCCCTGGCCAGTCTCCACAGTCCCTCATCTATGGATTTCCACAGATT	260

QY 241 TCTGGGTTGCCAGACAGGTTTCAGTGGCAGTTCAGGGACAGATTTCACACTCAGATC 300
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Db 261 TCTGGGTTGCCAGACAGGTTTCAGTGGCAGTTCAGGGACAGATTTCACACTCAGATC 320
|||
QY 301 TCCGAGTTAGAGGCTGAGAGCGTGGAGTGTATTACTGCTTACAAGGTACACATCAGCCG 360
|||
Db 321 AGCAGAGTGGAGGCTGAGATCTGGAGTTTATTCTGCTCTCAAGTACACATGTTCCG 380
|||
QY 361 TACAGTTTCGACAGGGGACCAAGTGGAAATATAA 396
|||
Db 381 TATACGTTGAGATCGGGACCAAGTGGAAATATAA 416
|||

Search completed: May 11, 1999, 12:00:35
Job time: 1482 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 11:44:16 ; Search time 479.58 Seconds
(without alignments)
1313.650 Million cells updates/sec

Title: US-08-700-737-20

Perfect score: 413
Sequence: 1 ATGAGTTCCTGTAGGCT.....AAACGGCTGATGCGCGCC 413

Scoring table: IDENTITY_NDC

Searched: 2002476 seqs, 762712212 residues

Database :

EST.*
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2: em_est2:*
3: em_est3:*
4: em_est4:*
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6: em_est6:*
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9: em_est9:*
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40: em_est18:*
41: em_est19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	237.2	57.4	488	11	H25625	H25625 y148905.r1

3	227.4	55.1	363	20	AA464313	AA464313 zx78c12.r
4	215.4	52.2	467	11	H27034	H27034 y165d05.r1
5	200.4	48.5	374	24	AA602059	AA602059 no95b02.s
6	192.6	46.6	357	11	T29104	T29104 EST69270 Ho
7	191.8	46.4	359	11	T27587	T27587 EST100475 H
8	183.4	44.4	430	12	H69156	H69156 y786f06.r1
9	182.8	44.3	335	24	AA402204	AA402204 zu46f03.r
10	179.4	43.4	287	21	AA496610	AA496610 zv38g06.r
11	177.2	42.9	445	10	R48141	R48141 y166c09.r1
12	160.4	38.8	470	12	H62115	H62115 y140p01.r1
13	159	38.5	400	20	AA456778	AA456778 zw27f11.r
14	155.4	37.6	257	10	R51193	R51193 y171a07.r1
15	155.4	37.6	246	27	AA871804	AA871804 vq41c03.r
16	150.8	36.5	398	10	AA423447	AA423447 ve80a03.r
17	149.8	36.3	248	24	AA430449	AA430449 zw20f11.r
18	146.2	35.4	420	20	AT120005	AT120005 uc25e04.r
19	144	34.9	240	24	AA418046	AA418046 zv33c09.r
20	137.6	33.3	370	17	AA295093	AA295093 EST100400
21	137.2	33.2	353	10	T72954	T72954 yc65a09.r1
22	134.8	32.6	418	21	AA515239	AA515239 ng69c07.s
23	134	32.4	253	17	AA295941	AA295941 EST101165
24	132.6	32.1	403	18	AA345486	AA345486 EST51505
25	131	31.7	349	18	AA379044	AA379044 EST91999
26	130.8	31.7	383	11	T29516	T29516 EST99871 Ho
27	130.6	31.6	364	11	T27579	T27579 EST100049 H
28	130.2	31.5	393	11	T27593	T27593 EST100653 H
29	129.4	31.3	413	17	AA301347	AA301347 EST14279
30	128.8	31.2	328	17	AA295311	AA295311 EST100471
31	127	30.8	405	18	AA360223	AA360223 EST69341
32	126.6	30.7	339	25	AA710249	AA710249 vt49e01.r
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35	123.6	29.9	338	17	AA321464	AA321464 EST23940
36	121.8	29.5	300	17	AA300994	AA300994 EST13943
37	120	29.1	363	17	AA300651	AA300651 EST13764
38	119	28.8	405	10	R48845	R48845 y165f10.r1
39	118.6	28.7	262	18	AA377807	AA377807 EST90452
40	118.2	28.6	346	17	AA300582	AA300582 EST13427
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ALIGNMENTS

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DEFINITION Scores ovary tumor N8HOT Homo sapiens CDNA clone 741987
(HUMAN); mRNA sequence.
5' similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II REGION
(HUMAN); mRNA sequence.
ACCESSION AA405415
NID 92063652
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 442)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-MCI human EST Project
Unpublished (1997)
TITLE JOURNAL
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

U, 3a, 3b, 3c, 3d, 3e, 3f, 3g, 3h, 3i, 3j, 3k, 3l, 3m, 3n, 3o, 3p, 3q, 3r, 3s, 3t, 3u, 3v, 3w, 3x, 3y, 3z, 3aa, 3ab, 3ac, 3ad, 3ae, 3af, 3ag, 3ah, 3ai, 3aj, 3ak, 3al, 3am, 3an, 3ao, 3ap, 3aq, 3ar, 3as, 3at, 3au, 3av, 3aw, 3ax, 3ay, 3az, 3ba, 3bb, 3bc, 3bd, 3be, 3bf, 3bg, 3bh, 3bi, 3bj, 3bk, 3bl, 3bm, 3bn, 3bo, 3bp, 3bq, 3br, 3bs, 3bt, 3bu, 3bv, 3bw, 3bx, 3by, 3bz, 3ca, 3cb, 3cc, 3cd, 3ce, 3cf, 3cg, 3ch, 3ci, 3cj, 3ck, 3cl, 3cm, 3cn, 3co, 3cp, 3cq, 3cr, 3cs, 3ct, 3cu, 3cv, 3cw, 3cx, 3cy, 3cz, 3da, 3db, 3dc, 3dd, 3de, 3df, 3dg, 3dh, 3di, 3dj, 3dk, 3dl, 3dm, 3dn, 3do, 3dp, 3dq, 3dr, 3ds, 3dt, 3du, 3dv, 3dw, 3dx, 3dy, 3dz, 3ea, 3eb, 3ec, 3ed, 3ee, 3ef, 3eg, 3eh, 3ei, 3ej, 3ek, 3el, 3em, 3en, 3eo, 3ep, 3eq, 3er, 3es, 3et, 3eu, 3ev, 3ew, 3ex, 3ey, 3ez, 3fa, 3fb, 3fc, 3fd, 3fe, 3ff, 3fg, 3fh, 3fi, 3fj, 3fk, 3fl, 3fm, 3fn, 3fo, 3fp, 3fq, 3fr, 3fs, 3ft, 3fu, 3fv, 3fw, 3fx, 3fy, 3fz, 3ga, 3gb, 3gc, 3gd, 3ge, 3gf, 3gg, 3gh, 3gi, 3gj, 3gk, 3gl, 3gm, 3gn, 3go, 3gp, 3gq, 3gr, 3gs, 3gt, 3gu, 3gv, 3gw, 3gx, 3gy, 3gz, 3ha, 3hb, 3hc, 3hd, 3he, 3hf, 3hg, 3hi, 3hj, 3hk, 3hl, 3hm, 3hn, 3ho, 3hp, 3hq, 3hr, 3hs, 3ht, 3hu, 3hv, 3hw, 3hx, 3hy, 3hz, 3ia, 3ib, 3ic, 3id, 3ie, 3if, 3ig, 3ih, 3ii, 3ij, 3ik, 3il, 3im, 3in, 3io, 3ip, 3iq, 3ir, 3is, 3it, 3iu, 3iv, 3iw, 3ix, 3iy, 3iz, 3ja, 3jb, 3jc, 3jd, 3je, 3jf, 3jg, 3jh, 3ji, 3jj, 3jk, 3jl, 3jm, 3jn, 3jo, 3jp, 3jq, 3jr, 3js, 3jt, 3ju, 3jv, 3jw, 3jx, 3jy, 3jz, 3ka, 3kb, 3kc, 3kd, 3ke, 3kf, 3kg, 3kh, 3ki, 3kj, 3kk, 3kl, 3km, 3kn, 3ko, 3kp, 3kq, 3kr, 3ks, 3kt, 3ku, 3kv, 3kw, 3kx, 3ky, 3kz, 3la, 3lb, 3lc, 3ld, 3le, 3lf, 3lg, 3lh, 3li, 3lj, 3lk, 3ll, 3lm, 3ln, 3lo, 3lp, 3lq, 3lr, 3ls, 3lt, 3lu, 3lv, 3lw, 3lx, 3ly, 3lz, 3ma, 3mb, 3mc, 3md, 3me, 3mf, 3mg, 3mh, 3mi, 3mj, 3mk, 3ml, 3mm, 3mn, 3mo, 3mp, 3mq, 3mr, 3ms, 3mt, 3mu, 3mv, 3mw, 3mx, 3my, 3mz, 3na, 3nb, 3nc, 3nd, 3ne, 3nf, 3ng, 3nh, 3ni, 3nj, 3nk, 3nl, 3nm, 3nn, 3no, 3np, 3nq, 3nr, 3ns, 3nt, 3nu, 3nv, 3nw, 3nx, 3ny, 3nz, 3oa, 3ob, 3oc, 3od, 3oe, 3of, 3og, 3oh, 3oi, 3oj, 3ok, 3ol, 3om, 3on, 3oo, 3op, 3oq, 3or, 3os, 3ot, 3ou, 3ov, 3ow, 3ox, 3oy, 3oz, 3pa, 3pb, 3pc, 3pd, 3pe, 3pf, 3pg, 3ph, 3pi, 3pj, 3pk, 3pl, 3pm, 3pn, 3po, 3pp, 3pq, 3pr, 3ps, 3pt, 3pu, 3pv, 3pw, 3px, 3py, 3pz, 3qa, 3qb, 3qc, 3qd, 3qe, 3qf, 3qg, 3qh, 3qi, 3qj, 3qk, 3ql, 3qm, 3qn, 3qo, 3qp, 3qq, 3qr, 3qs, 3qt, 3qu, 3qv, 3qw, 3qx, 3qy, 3qz, 3ra, 3rb, 3rc, 3rd, 3re, 3rf, 3rg, 3rh, 3ri, 3rj, 3rk, 3rl, 3rm, 3rn, 3ro, 3rp, 3rq, 3rr, 3rs, 3rt, 3ru, 3rv, 3rw, 3rx, 3ry, 3rz, 3sa, 3sb, 3sc, 3sd, 3se, 3sf, 3sg, 3sh, 3si, 3sj, 3sk, 3sl, 3sm, 3sn, 3so, 3sp, 3sq, 3sr, 3ss, 3st, 3su, 3sv, 3sw, 3sx, 3sy, 3sz, 3ta, 3tb, 3tc, 3td, 3te, 3tf, 3tg, 3th, 3ti, 3tj, 3tk, 3tl, 3tm, 3tn, 3to, 3tp, 3tq, 3tr, 3ts, 3tt, 3tu, 3tv, 3tw, 3tx, 3ty, 3tz, 3ua, 3ub, 3uc, 3ud, 3ue, 3uf, 3ug, 3uh, 3ui, 3uj, 3uk, 3ul, 3um, 3un, 3uo, 3up, 3uq, 3ur, 3us, 3ut, 3uu, 3uv, 3uw, 3ux, 3uy, 3uz, 3va, 3vb, 3vc, 3vd, 3ve, 3vf, 3vg, 3vh, 3vi, 3vj, 3vk, 3vl, 3vm, 3vn, 3vo, 3vp, 3vq, 3vr, 3vs, 3vt, 3vu, 3vv, 3vw, 3vx, 3vy, 3vz, 3wa, 3wb, 3wc, 3wd, 3we, 3wf, 3wg, 3wh, 3wi, 3wj, 3wk, 3wl, 3wm, 3wn, 3wo, 3wp, 3wq, 3wr, 3ws, 3wt, 3wu, 3wv, 3ww, 3wx, 3wy, 3wz, 3xa, 3xb, 3xc, 3xd, 3xe, 3xf, 3xg, 3xh, 3xi, 3xj, 3xk, 3xl, 3xm, 3xn, 3xo, 3xp, 3xq, 3xr, 3xs, 3xt, 3xu, 3xv, 3xw, 3xx, 3xy, 3xz, 3ya, 3yb, 3yc, 3yd, 3ye, 3yf, 3yg, 3yh, 3yi, 3yj, 3yk, 3yl, 3ym, 3yn, 3yo, 3yp, 3yq, 3yr, 3ys, 3yt, 3yu, 3yv, 3yw, 3yx, 3yy, 3yz, 3za, 3zb, 3zc, 3zd, 3ze, 3zf, 3zg, 3zh, 3zi, 3zj, 3zk, 3zl, 3zm, 3zn, 3zo, 3zp, 3zq, 3zr, 3zs, 3zt, 3zu, 3zv, 3zw, 3zx, 3zy, 3zz, 4a, 4b, 4c, 4d, 4e, 4f, 4g, 4h, 4i, 4j, 4k, 4l, 4m, 4n, 4o, 4p, 4q, 4r, 4s, 4t, 4u, 4v, 4w, 4x, 4y, 4z, 5a, 5b, 5c, 5d, 5e, 5f, 5g, 5h, 5i, 5j, 5k, 5l, 5m, 5n, 5o, 5p, 5q, 5r, 5s, 5t, 5u, 5v, 5w, 5x, 5y, 5z, 6a, 6b, 6c, 6d, 6e, 6f, 6g, 6h, 6i, 6j, 6k, 6l, 6m, 6n, 6o, 6p, 6q, 6r, 6s, 6t, 6u, 6v, 6w, 6x, 6y, 6z, 7a, 7b, 7c, 7d, 7e, 7f, 7g, 7h, 7i, 7j, 7k, 7l, 7m, 7n, 7o, 7p, 7q, 7r, 7s, 7t, 7u, 7v, 7w, 7x, 7y, 7z, 8a, 8b, 8c, 8d, 8e, 8f, 8g, 8h, 8i, 8j, 8k, 8l, 8m, 8n, 8o, 8p, 8q, 8r, 8s, 8t, 8u, 8v, 8w, 8x, 8y, 8z, 9a, 9b, 9c, 9d, 9e, 9f, 9g, 9h, 9i, 9j, 9k, 9l, 9m, 9n, 9o, 9p, 9q, 9r, 9s, 9t, 9u, 9v, 9w, 9x, 9y, 9z, 10a, 10b, 10c, 10d, 10e, 10f, 10g, 10h, 10i, 10j, 10k, 10l, 10m, 10n, 10o, 10p, 10q, 10r, 10s, 10t, 10u, 10v, 10w, 10x, 10y, 10z, 11a, 11b, 11c, 11d, 11e, 11f, 11g, 11h, 11i, 11j, 11k, 11l, 11m, 11n, 11o, 11p, 11q, 11r, 11s, 11t, 11u, 11v, 11w, 11x, 11y, 11z, 12a, 12b, 12c, 12d, 12e, 12f, 12g, 12h, 12i, 12j, 12k, 12l, 12m, 12n, 12o, 12p, 12q, 12r, 12s, 12t, 12u, 12v, 12w, 12x, 12y, 12z, 13a, 13b, 13c, 13d, 13e, 13f, 13g, 13h, 13i, 13j, 13k, 13l, 13m, 13n, 13o, 13p, 13q, 13r, 13s, 13t, 13u, 13v, 13w, 13x, 13y, 13z, 14a, 14b, 14c, 14d, 14e, 14f, 14g, 14h, 14i, 14j, 14k, 14l, 14m, 14n, 14o, 14p, 14q, 14r, 14s, 14t

2

an.

• 176 •

0; Gadps


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RESULT 3
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DEFINITION 5' similar to gb:x72467 IG KAPPA CHAIN PRECURSOR V-II REGION
(HUMAN); mRNA sequence.
ACCESSION AA464313
NID 92189197
KEYWORDS EST. human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 363)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theisling,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m1 rev2 ET from Amerham.
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TGTTCACATCTGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
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the Not I and Eco RI sites of a modified p7773 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
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Matches 276; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
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DB 5 CTGATTCACAGTGGGATATGATGATGATGATGATGATGATGATGATGATGATGATG 64
QY 107 GAGAACAGCTTCTATCTCTTGAAGTCTGATGATGATGATGATGATGATGATGATGATG 166
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DB 65 GAGAGCGGCTCTCATCTCTGCAAGTCTGATGATGATGATGATGATGATGATGATGAT 124
QY 167 CCTATTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 226
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DB 125 ACTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 184
QY 227 TTTCACACAGATTTTCTGGGGTGCACAGAGTTCACTGTCAGTGTTCAGGAGCAGATT 286

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Db 185 GTTCTATCGGGCCCTCGGGGCTCCCTGACAGGTTCACTGATGATGATGATGATGATG 244
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DB 245 TTACACTGAAATATCAGCAGAGTGTAGAGCTGTAGAGCTGTAGAGCTGTAGAGCTGTAG 304
QY 347 GTACACATCAGCCCTACAGCTTTCGACAGGAGGAGCAAGTGTAAATATAACGGGCTG 403
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DB 305 CTCTACAACCTTATTCACCTTTCGGCCCTGGACCAAGTGTATCAACAGCACTG 361
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LOCUS Y165d05.r1 Homo sapiens cDNA clone 163113 5' similar to gb:x72467
DEFINITION IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);
ACCESSION H27034
NID 9897024
KEYWORDS EST.
SOURCE human clone-163113 library-Soares breast 3NDBst vector-p7773D
(Pharmacia) with a modified polylinker host-DH10B (ampicillin
resistant) primer-M13Rpl Rsite1-Not I Rsite2-Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adapters (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified p7773 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 467)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,R., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisan,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
High quality sequence steps: 352
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
LOCATION/Qualifiers
1..467
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/clone="163113"
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Best Local Similarity 76.5%; Pred. No. 2.2e-57;
Matches 264; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
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111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 3 ATGAGGCTCCCTCTCAAGCTCTGAGGCTGCTAATCTCTGAGTCTGTGATTCAGTGGG 62
QY 61 GATGTTGTGATGATCAAGTCCACTCTCCCTGCTGTCACCCCTGAGAACAGCTTCT 120
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

```

Db 63 GATATTGATGACTCACTCCACTCTCCAGCCGCTACCCCTCGAGAGCCGCTCC 122
 QY 121 ATCTTGAGAGTGTAGTCAAGAGTTCGAAAGATTATGGAGACCATTTGCTGG 180
 Db 123 ATCTCTGCAAGTCTAGTCAAGGCTCTACATAGTATGATGATGATTTGATTGG 182
 QY 181 TACCTGCAAGAGCTGCGGCTCTCCAGAGCTCTCATCTATGAGATTTCAGAGATT 240
 Db 183 TACCTGCAAGAGCTGCGGCTCTCCAGAGCTCTCATCTATGAGATTTCAGAGATT 242
 QY 241 TCTGGGGTCCAGACAGTTCAGTGGAGTGTTCAGGAGACAGATTTCACACTCAATC 300
 Db 243 TCCGGGCTCCAGAGTTCAGTGGAGTGTTCAGGAGACAGATTTCACACTCAATC 302
 QY 301 TCCGAGTAGAGCTGAGAGCTGGAGTGTATTACTCTTACCA 345
 Db 303 AGTAGAGTAGAGCTGAGAGTGTATTACTCTTACCA 347

RESULT 5
 AA602059 374 bp mRNA EST 08-OCT-1997
 LOCUS 095B02.S1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1114539
 DEFINITION similar to gb:X53400.cds1 IG KAPPA CHAIN PRECURSOR V-II REGION
 (HUMAN): contains Alu repetitive element; mRNA sequence.

ACCESSION
 AA602059
 NID 92435848
 KEYWORDS EST.

SOURCE
 ORGANISM human.

REFERENCE
 AUTHORS Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homiidae; Homo.
 TITLE 1 (bases 1 to 374)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT

Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai,
 M.D., Michael Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Kitzman, Ph.D.
 DNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LML at:
 www-bio.liml.gov/bdip/image/image.html

Insert Length: 1123 Std Error: 0.00
 Seq primer: -40ml3 fwd. fr from Amersham
 High quality sequence step: 369.

FEATURES
 SOURCE Location/Qualifiers

1. 374
 /organism="Homo sapiens"
 /note="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from
 5,000-10,000 microdissected preneoplastic cells
 histologically-determined to be prostatic intraepithelial
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the
 cDNA with an adaptor-specific primer and the resulting
 PCR product subcloned into pAMP10 by the UBC-cloning
 method (Life Technologies). Average insert size is 600
 bp. NOTE: Not directionally cloned. This library was
 constructed by David Kitzman."
 /db_xref="taxon:9606"
 /clone="IMAGE:1114539"
 /clone_lib="NCI_CGAP_P22"
 /sex="Male"
 /dev_stage="45 years old"

BASE COUNT 78 a 105 c 102 g 89 t
 ORIGIN

Query Match 48.5%; Score 200.4; DB 24; Length 374;
 Best Local Similarity 73.7%; Pred. No. 1e-52;
 Matches 255; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1 ATGAGTTGCTGTTAGGCTGTGCTCTCTCTGTTTCTGAGATTCCTGTTCCGAGGT 60
 Db 29 ATGAGGCTCTCTGCTCAAGTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 88
 QY 61 GATGTTGATGATCAAGTCTCACTCTCCCTGCTCTCAACCCCTGAGAGACAGTCTT 120
 Db 89 GATATGAGTAGACCAAGACAGTCTCTCTCACTCTCAACCCCTGAGAGACAGTCTT 148
 QY 121 ATCTCTGAGAGTCTAGTCAAGTCTTTCGAAAGAGTATGGGAACACCTATTGCTTGG 180
 Db 149 ATCTCTGAGAGTCTAGTCAAGTCTTTCGAAAGAGTATGGGAACACCTATTGCTTGG 208
 QY 181 TACCTGAGAGAGCTGCGGCTCTCCAGAGCTCTCTCATATGAGATTTCACAGATT 240
 Db 209 CTGACCAAGAGCCAGGCTGAGCTCTCCAGAGCTCTCATATGAGATTTCACAGATT 268
 QY 241 TCTGGGGTCCAGACAGTTCAGTGGAGTGTTCAGGAGACAGATTTCACACTCAATC 300
 Db 269 TCTGGGGTCCAGACAGTTCAGTGGAGTGTTCAGGAGACAGATTTCACACTCAATC 328
 QY 301 TCCGAGTAGAGCTGAGAGCTGGAGTGTATTACTCTTACCA 346
 Db 329 AGTAGAGTAGAGCTGAGAGTGTATTACTCTTACCA 374

RESULT 6
 LOCUS T29104 357 bp mRNA EST 06-SEP-1995
 DEFINITION EST69270 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
 light chain V region (GB:X54248) (HT:3095).
 T29104
 NID 9611202
 KEYWORDS EST.

SOURCE
 ORGANISM human primer-M13 Reverse library=Human Lymphoid tissue.

REFERENCE
 AUTHORS Homo sapiens
 Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 357)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bull,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chui,M.-W.,
 Clayton,R.A., Cline,R.T., Cotton,M.D., Eale,Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S.M.,
 Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S.,
 Kelley,J.M., Kline,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
 Merrick,J.M., Moreno-Palancues,R.F., McDonald,L.A., Nguyen,D.T.,
 Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
 Sudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Ulterbeck,T.R.,
 Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
 Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferlie,A.,
 Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
 Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
 Meisner,P.S., Olsen,H., Raymond,L., Weli,Y.-F., Wing,J., Xu,C.,
 Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,W.R., Rosen,C.A.,
 Haseltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C.
 Initial Assessment of Human Gene Diversity and Expression Patterns
 Based Upon 52 Million Basepairs of cDNA Sequence
 Unpublished (1995)

JOURNAL
 COMMENT Other_ESTs: EST69269
 Contact: Venter, JC
 The Institute for Genomic Research
 932 Clopper Rd, Galtherburg, MD 20878

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 430)

HILLIER, L., CLARK, N., DUBUQUE, T., ELLISTON, K., HAWKINS, M.,

Query Match	38.5%;	Score 159;	DB 20;	Length 400;
Best Local Similarity	67.1%;	Pred. No. 9,5e+40;		
Matches 261;	Conservative	0;	Mismatches 115;	Indels 13;
				Gaps 2

RESULT	14
R51193	
LOCUS	R51193
DEFINITION	R51193 257 bp mRNA EST 18-MAY-1995
DESCRIPTION	yj71a07.r1 Homo sapiens cDNA clone 154164 5' similar to gb:U72467
ACCESSION	IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN)).

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
Homio saplens				
Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Saccopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.				
1 (bases 1 to 257)				
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Holtman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Pearson, D., Rifkin, L., Rohlfing, T., Soares, M., Tar, F., Trevaschik, E., Waterston, R., Willamson, A., Wohlmann, P. and Wilson, R.				
The Washu-Merck EST Project				
Unpublished (1995)				

FEATURES	BASE COUNT	ORIGIN
source	53 a	67 c 62 g 63 t 12 others
location/qualifiers		
1.257		
/organism="Homo sapiens"		
/clone="154164"		
Query Match	37.6%	Score 155.4; DB 10; Length 257;
Best Local Similarity	73.5%	Pred. No. 1.1e-38;
Matches 189; Conservative	0;	Mismatches 68; Indels 0; Gaps 0
0Y	70	ATGACTCAAGGCCACTCTCCCTGGCTGTGACCCCTGGAGAACAGACTCTATCTTTCG 129
Db	1	AMGACTCANTCTCCACTCTCCCTGGCCCGGACCCCTGGNAGCCNCCCTCCATCTCTTCG 60
0Y	130	AGGCTAGTCAGAGTCTTTCGAAAGATTATGGAAACACCTATTGTCCTGTACCTGCAG 189
Db	61	AGGCTAGTCAGAGGCTCTCTGAGATATGATATTAATATTATTTAGATTGTGACCTGCAG 120
0Y	190	AAGCTGGCCACTCTCCACAGTCTCTCATCTATGGATTTCCACAGATTTCTGGGGTG 249
Db	121	AGGCCANAGCGGCTCNCACAACTCTGTATCTCTTGGCTTAAACGGGCGCTTCGGGGNC 180
0Y	250	CCAGCAGAGTTCAGTGGAGTGTGTGACAGGAGATTTCCACTCAAGTACCTGGAGAGA 309
Db	181	CCTGACAGTTCAGTGGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 240
0Y	310	GAGGCTGAGAGCGATGGG 326
Db	241	GANGCTGAGAGTGTGG 257
RESULT 15		
AA871804		
LOCUS	AA871804	246 bp mRNA EST 16-MAR-1998
DEFINITION	vq41c03.1	Barcode bowel MLEB9 Mus musculus cDNA clone 1096804 5
		Similar to gb:U72431 IG KAPPA CHAIN V-II REGION (HUMAN).; mRNA
sequence.		
ACCESSION	AA871804	
NID	92967249	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryotes: Metazoa: Chordata: Vertebrata; Mammalia: Eutheria;	
AUTHORS	Rodentia: Scurionath; Muridae; Murinae; Mus.	
	1 (bases 1 to 246)	
	Maria, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,	
	Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,	
	Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,	
	Teising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and	
	Washington, R.	
TITLE	The WashU-HMI Mouse EST Project	
JOURNAL	Unpublished (1996)	
COMMENT		
	Contact: Maria M/Mouse EST Project	
	WashU-HMI Mouse EST Project	
	Washington University School of Medicine	
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
	Tel: 314 286 1800	
	Fax: 314 286 1810	
	Email: mouseest@wustl.edu	
	This clone is available royalty-free through LNL; contact the	
	IMAGE Consortium (info@image.llnl.gov) for further information.	
	MI:603036	
	Seq primer: -26m13 rev2 EF from Amer sham.	
FEATURES	Location/Qualifiers	
source	1.246	
	/organism="Mus musculus"	
	/strain="FVB/N"	
	/note="Vector: pT73D-Pac (Pharmacia) with a modified	

polylinker: Site.1: EcoRI; Site.2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dN) primer [5'
TCTTACGATCTGAGGAGGAGGCGCCGCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT73 vector.
Source irradiated bowel harvested 72 hours after
irradiation (1400 Gys). Library constructed by Bob
Birstead "

/db_xref="taxon:10090"
/clone="1096804"
/clone_lib="Birstead bowel MPLRB9"
/tissue_type="bowel"
/dev_stage="8 weeks"
/lab_host="DH10B"

BASE COUNT 59 a 66 c 51 g 70 t
ORIGIN

Query Match 37.6%; Score 155.4; DB 27; Length 246;
Best Local Similarity 82.7%; Pred. No. 1.1e-38;
Matches 191; Conservative 0; Mismatches 36; Indels 4; Gaps 1;

QY 1 ATGAGTGCCTGTAGGCTGTGGCTTCTGTGTTGATTCCTGTTCCGAGGT 60
|||||
DB 20 ATGAGTGCCTGTAGGCTGTGGCTGTGGCTGTGATTCCTGTTCCGAGGT 75
|||||
QY 61 GATGTGTGATGATCAAGATCCACTCCCTGCTGACCCCGAGAACCAAGCTCT 120
|||||
DB 76 GATGTGTGATGATCAAGATCCACTCCCTGCTGACCTGTGAGATCAAGCTCT 135
|||||
QY 121 ATCTCTCAGGTCTAGTCAGAGTCTTCAAGAGTATGAGAACCTATTTGCTTGG 180
|||||
DB 136 ATCTCTCAGGTCTAGTCAGAGTCTTCAAGAGTATGAGAACCTATTTGCTTGG 195
|||||
QY 181 TACCTGCAGAAAGCTGTCCACAGCTCTCATCTATGAGATTTC 231
|||||
DB 196 TACCTGCAGAAAGCTGTCCACAGCTCTCATCTATGAGATTTC 246
|||||

Search completed: May 11, 1999, 11:44:17
Job time: 504 sec

OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 12:03:35 ; Search time 88.51 Seconds
(about 34 minutes)

(without alignments)
877.846 Million cell updates/sec

Title: US-08-700-737-20

Sequence: 1 ATGAGTGCCTGTTAGCT...AACGGCTGATGCGGCC 413

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database : N_Geneseq_34 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	411.4	99.6	413	1	V20075	DNA encoding the 1
2	374.6	90.7	535	1	V20086	Consensus DNA sequ
3	360.8	87.4	396	1	V20077	DNA encoding murin
4	299.4	72.5	717	1	T62934	Murine anti-porcine
5	299.4	72.5	5300	1	T62938	3F4 human IgG4 exp
6	297.8	72.1	537	1	Q14651	R6-5-D6 anti-ICAM-
7	294.6	71.3	394	1	Q62803	Humanised murine F
8	294.6	71.3	394	1	Q87533	Humanised anti-KC-
9	294.6	71.3	717	1	T88870	L chain subunit O6
10	294.6	71.3	717	1	V66736	Anti-human Fas mon
11	293	70.9	537	1	Q14801	Encodes murine anti
12	293	70.9	447	1	T31332	Anti-idiotypic monoc
13	291.4	70.6	394	1	Q62790	Humanised murine B
14	286.6	69.4	394	1	Q62763	Murine KC-4 immuno
15	286.6	69.4	394	1	Q62788	Murine KC-4 immuno
16	286.6	69.4	420	1	V60831	Variable light cha
17	286	69.2	427	1	Q36529	Chimeric MAb ligh
18	286	69.2	427	1	Q36536	BR5-2 light chain
19	285	69.0	394	1	Q87531	VL sequence of anti
20	283.4	68.9	424	1	T98835	Coding sequence fo
21	283.8	68.7	396	1	V37255	cDNA encoding a va
22	283.4	68.6	394	1	Q62774	Murine BRE-3 immu
23	283.4	68.6	394	1	Q62774	Murine BRE-3 immu
24	282.8	68.5	8897	1	V18692	Plasmid pTWD-CpV
25	282.4	68.4	434	1	Q36534	BR5-2 murine IgG3
26	281.2	68.1	384	1	V56333	Murine ICR-8.1 V-K
27	281.2	68.1	384	1	V54852	Murine antibody IC
28	280	67.8	489	1	Q11282	Encodes murine mo
29	278.6	67.5	388	1	V66674	Anti-Fas MAb CH11
30	273.2	66.2	422	1	V20705	DNA encoding the 1
31	272.8	66.1	432	1	Q80606	Co-1 light chain V
32	272.8	66.1	861	1	Q81500	sFV anti-rev sequen
33	272.8	66.1	432	1	T43439	MAb Co-1 light cha
34	272.8	65.1	861	1	T45347	Single chain sFV a
35	269	65.1	720	1	V61359	Anti-human Fas hum
36	267.4	64.7	720	1	V61360	Anti-human Fas hum
37	267.4	64.7	720	1	V61361	Anti-human Fas hum
38	266.8	64.6	8897	1	V18693	Plasmid pDI6hJ1.L
39	266	64.4	375	1	V56402	Human ICR-8.1 V-K
40	265.8	64.4	375	1	V54860	Humanised murine a
41	265.8	64.4	720	1	V61382	Anti-human Fas hum
42	261.2	63.2	330	1	Q43746	Sequence encoding
43	257	62.2	782	1	Q86755	Anti-dansyl single

ALIGNMENTS

44	253.8	61.5	876	1	V10390	Monoclonal antibody
45	250.8	60.7	699	1	T16700	Lewis-Y antibody B

```

RESULT      1
V20075
ID          V20075 standard; DNA: 413 BP.
AC          V20075.
DT          14-JUL-1998 (first entry)
DE          DNA encoding the light chain of a humanised murine Act-1 antibody.
KW          Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW          Muscosal adressin cell adhesion molecule-1; MacCAM-1;
KW          humanised antibody; murine antigen binding region; inhibition;
KW          leucocyte infiltration of tissue; treatment; inflammatory disease;
KW          inflammatory bowel disease; ss.
OS          Homo sapiens.
FH          Key
FT          CDS
FT          sig_peptide
FT          mat_peptide
FT          sig_peptide
FT          mat_peptide
FT          sig_peptide
FT          mat_peptide
PN          WO9806248-A2.
PD          19-FEB-1998.
PF          06-AUG-1997; U13884.
PR          15-AUG-1996; US-700737.
PI          (LEUK-) LEUCOSITE INC.
PI          Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
PI          Saldanha J;
DR          MPI; 98-159172/14.
DR          P-PADB; W53812.
PT          Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
PT          used for treating inflammatory disease, pancreatitis, diabetes,
PT          asthma, graft versus host disease and sarcoidosis
PS          Claim 17; Fig 12; 145pp; English.
CC          The present sequence encodes the light chain of humanised murine
CC          antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
CC          Muscosal adressin cell adhesion molecule-1 (MacCAM-1) is a ligand of
CC          this particular integrin. The Act-1 antibody interferes with alpha4-beta7
CC          Integrin binding to MacCAM-1, which is present of high endothelial
CC          venules in muscosal lymph nodes. The humanised immunoglobulin can be
CC          used to inhibit the interaction of cells bearing alpha4-beta7 with
CC          cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
CC          leukocyte infiltration of tissues, e.g. for treating inflammatory
CC          diseases such as inflammatory bowel disease. The immunoglobulin can
CC          also be used for detection, isolation and diagnosis.
SQ          Sequence 413 BP; 90 A; 96 C; 116 G; 111 T;

Query Match          99.6%; Score 411.4; DB 1; Length 413;
Best Local Similarity 99.8%; Pred. No. 2,2e+127;
Matches 412; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

OY    1 ATGAAGTTGCCCTGATAGCGCTGTGGTGCCTTCCTGTTCTGGATTCCCTTTCCGGAGGT 60
DB    1 ATGAAGTTGCCCTGATAGCGCTGTGGTGCCTTCCTGTTCTGGATTCCCTTTCCGGAGGT 60

OY    61 GATGTGTGATGACTCAAAAGTCCACTCTCCCTGCCTGATCACCCTTGAGAACCAAGCTTCT 120
DB    61 GATGTGTGATGACTCAAAAGTCCACTCTCCCTGCCTGATCACCCTTGAGAACCAAGCTTCT 120

OY    121 ATCTCTTGAGAGGTCTAAGTCAGAGCTCTTGAAGAAGACTTAAAGGAACAACCATTTGCTTGG 180
DB    121 ATCTCTTGAGAGGTCTAAGTCAGAGCTCTTGAAGAAGACTTAAAGGAACAACCATTTGCTTGG 180

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QY 181 TACCTGCAGAAAGCTGCGCAGCTCTCCACAGCTCTCATCTATGAGATTTCACAGATTT 240
 Db 181 TACCTGCAGAAAGCTGCGCAGCTCTCCACAGCTCTCATCTATGAGATTTCACAGATTT 240
 QY 241 TCTGGGGTCCAGACAGGTTGAGTGGCAGTGGTTTCAGGAGACAGATTTCACACTCAAGTC 300
 Db 241 TCTGGGGTCCAGACAGGTTGAGTGGCAGTGGTTTCAGGAGACAGATTTCACACTCAAGTC 300
 QY 301 TCGGAGTAGAGGCTGAGAGCTGGAGTGTATCTACTCTTACAGATTCACATCAGCCG 360
 Db 301 TCGGAGTAGAGGCTGAGAGCTGGAGTGTATCTACTCTTACAGATTCACATCAGCCG 360
 QY 361 TACACGTTCCGACAGGGGACCAAGGTGAATAAAGCGGCTGATGCGCGCC 413
 Db 361 TACACGTTCCGACAGGGGACCAAGGTGAATAAAGCGGCTGATGCGCGCC 413

RESULT 2
 V20086
 ID V20086 standard; DNA; 535 BP.
 AC V20086;
 DT 14-JUL-1998 (first entry)
 DE Consensus DNA sequence of the murine variable light chain region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised adressin cell adhesion molecule-1; MadCAM-1;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 OS Mus sp.
 FH Key
 FT CDS Location/Qualifiers
 FT 16..435
 FT /tag= a
 FT /note= "no stop codon given"
 FT sig_peptide
 FT 16..75
 FT /tag= b
 FT mat_peptide
 FT 76..435
 FT /tag= c

WO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ, Saldanha J;
 DR WPI: 98-159172/14.
 DR P-PSDB: W53817.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 3; 145pp; English.
 CC The present sequence represents the consensus nucleotide sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse light chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal adressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in muscosal
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20083-84. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 535 BP; 126 A; 128 C; 132 G; 149 T;

Matches 389; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 1 ATGAGATTGCTGTAGAGCTGTGTGCTCTCTGTCTTCTTGATTCCTGTTCCGAGGT 60
 Db 16 ATGAGTTGCTGTAGAGCTGTGTGCTCTCTGTCTTCTTGATTCCTGTTCCGAGGT 75
 QY 61 GATTTGTGATGACTCAAGTCCACTCTCCCTGCTGTCAACCCTGAGAACAGCTTCT 120
 Db 76 GATTTGTGAGTACTCAAACTCCACTCTCCCTGCTGTCAAGTGTGAGATCAAGTTCT 135
 QY 121 ATCTCTGACAGCTTACATCAGAGCTGTGCAAGAGTATGGAGACACTATTTGCTGG 180
 Db 136 ATCTCTGACAGCTTACATCAGAGCTGTGCAAGAGTATGGAGACACTATTTGCTGG 195
 QY 181 TACCTGCAGAAAGCTGCGCAGCTCTCCACAGCTCTCATCTATGAGATTTCACAGATTT 240
 Db 196 TACCTGCAGAAAGCTGCGCAGCTCTCCACAGCTCTCATCTATGAGATTTCACAGATTT 255
 QY 241 TCTGGGGTCCAGACAGGTTGAGTGGCAGTGGTTTCAGGAGACAGATTTCACACTCAAGTC 300
 Db 256 TCTGGGGTCCAGACAGGTTGAGTGGCAGTGGTTTCAGGAGACAGATTTCACACTCAAGTC 315
 QY 301 TCGGAGTAGAGGCTGAGAGCTGGAGTGTATCTACTCTTACAGATTCACATCAGCCG 360
 Db 316 AGCACATAAAGCTTGAGGACTTGGATGTATTACGCTTACAGGTACATCAGCCG 375
 QY 361 TACACGTTCCGACAGGGGACCAAGGTGAATAAAGCGGCTGATGCGCGCC 413
 Db 376 TACACGTTCCGACAGGGGACCAAGGTGAATAAAGCGGCTGATGCGCGCC 428

RESULT 3
 V20077
 ID V20077 standard; DNA; 396 BP.
 AC V20077;
 DT 14-JUL-1998 (first entry)
 DE DNA encoding murine Act-1 light chain variable region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised adressin cell adhesion molecule-1; MadCAM-1;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 OS Mus sp.
 FH Key
 FT CDS Location/Qualifiers
 FT 1..396
 FT /tag= a
 FT sig_peptide
 FT 1..60
 FT /tag= b
 FT mat_peptide
 FT 61..396
 FT /tag= c

WO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ, Saldanha J;
 DR WPI: 98-159172/14.
 DR P-PSDB: W53814.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Claim 26; Fig 7; 145pp; English.
 CC The present sequence encodes the light chain variable region of
 CC murine antibody Act-1. Act-1 is active against human alpha4-beta7
 CC integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a
 CC ligand of this particular integrin. The Act-1 antibody interferes with
 CC alpha4-beta7 integrin binding to MadCAM-1, which is present of high
 CC endothelial venules in muscosal lymph nodes. Humanised Act-1 can be used
 CC to inhibit the interaction of cells bearing alpha4-beta7 with cells
 CC bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can

Query Match: 90.7%; Score 374.6; DB 1; Length 535;
 Best local Similarity 94.2%; Pred. No. 4.1e-115;


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FT      Intron      /tag- k
FT      4234. 4463
FT      /tag- l
FT      4464. 5212
FT      /tag- m
FT      /codon_start- 4496
PN      MO9711971-A1.
PD      03-APR-1997.
PF      27-SEP-1996: U15575.
PR      28-SEP-1995: US-004489.
PR      26-SEP-1996: US-004489.
PA      (ALEX-) ALEXION PHARM INC.
PI      Evans MJ, Mats LA, Mueller EE, Mueller JP, Rollins S;
PI      Rother RP;
DR      WPI: 97-212855/19.
DR      P-PSDB: W14941.
DR      P-PSDB: W14942.
PT      Antibodies binding to porcine but not human cell interaction
PT      proteins - useful to treat and assay for rejection of xenografted
PT      porcine organs, tissues or cells
PS      Disclosure: Page 61-67: 105pp; English.
CC      A DNA sequence (T62938) comprises a 3f4 human IgG4 expression
CC      plasmid insert sequence. It is obtd. by cloning the light chain
CC      (see also T62934) and heavy chain (see also T62935) variable
CC      region sequences of murine anti-porcine vascular cell adhesion
CC      molecule (VCAM) monoclonal antibody 3f4 into an expression plasmid
CC      modified to contain the human gamma4 constant region in plasmid of
CC      the human gamma C1 region. The encoded heavy chain (W14941) and
CC      light chain (W14942) can be used to produce a chimeric antibody
CC      that is specific for porcine VCAM. The chimeric antibody is useful
CC      for diagnosing human rejection of porcine xenotransplants and for
CC      improving xenotransplantation of porcine cells, tissues and organs.
CC      into human recipients.
SQ      Sequence 5300 BP: 1236 A; 1494 C; 1375 G; 1195 T;

Query Match      72.5%; Score 299.4; DB 1; Length 5300;
Best Local Similarity 84.3%; Pred. No. 1e-89;
Matches 349; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY      1 ATGAAGTGGCTGTAGGCTGTGGTCTGTGTGTGTGAGTTCCTGTTCCGGAGGT 60
DB      4496 ATGAAGTGGCTGTAGGCTGTGGTCTGTGTGTGTGAGTTCCTGTTCCGGAGGT 4552
QY      61 GATGTGTGATGACTCAAGTCCACTCTCCCTGCTGTCAACCCCTGGAGAACAGCTTCT 120
DB      4553 GATGTGTGATGACTCAAGTCCACTCTCCCTGCTGTCAAGTTCGAGATCAAGCTCC 4612
QY      121 ATCTCTTGACAGGTCTAGTCAAGTCTTGCAAGAGATTATGGAAACCTTATTGTCTTG 180
DB      4613 ATCTCTTGACAGGTCTAGTCAAGTCTTGCAAGAGATTATGGAAACCTTATTGTCTTG 4672
QY      181 TACTGTGAGAAAGCTGGCCAGTCCACAGTCTCTCATCTATGAGATTCCACAGATT 240
DB      4673 TACTGTGAGAAAGCTGGCCAGTCCACAGTCTCTCATCTATGAGATTCCACAGATT 4732
QY      241 TCTGGGGTGCAGACAGGTTCAAGTCAAGTGTTCAGGAGACAGATTTCACACTCAAGATC 300
DB      4733 TCTGGGGTGCAGACAGGTTCAAGTGTTCAGGAGACAGATTTCACACTCAAGATC 4792
QY      301 TCGCGAGTAGAGCTGAGAGCTGGAGTGTATTACTGTCTTACAGGTACATCAACCG 360
DB      4793 AGCAGAGTGGAGCTGAGAGTCTGGAGTGTATTACTGTCTTACAGGTACATCAACCG 4852
QY      361 TACACGTTGGAGACAGGGGACCAAGGTGGAATAAAGGGCTGATGGGGGCC 413
DB      4853 TACACGTTGGAGACAGGGGACCAAGGTGGAATAAAGGGCTGATGGGGGCC 4905

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RESULT 6
 ID Q14651 standard; cDNA: 537 BP.
 AC Q14651;

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DT      14-FEB-1992 (first entry)
DE      R6-5-D6 anti-ICAM-1 light chain.
KW      Intercellular adhesion molecule-1; antibody; chimeric; ds.
OS      Mus musculus.
FH      Key signal_peptide 19..75
FT      Location/Qualifiers
FT      /tag- a
FT      19..537
FT      cds
FT      /tag- b
PN      MO9116928-A.
PD      14-NOV-1991.
PF      29-APR-1991: U02946.
PR      27-APR-1990: GB-009548.
PA      (CELL-) CELLTECH LTD.
PA      (BOEH) BOEHRINGER INGELHEIM PHA.
PI      Adair JR, Robinson MK, Bright SM, Rothlein RA;
PI      WPI: 91-353534/48.
DR      P-PSDB: R15199.
PT      New humanised chimeric anti-ICAM-1 antibodies - useful in
PT      treating inflammation e.g. psoriasis and ulcerative colitis to
PT      suppress metastasis of haematopoietic tumour cell and in
PT      diagnosis.
PS      Claim 10; Fig 1; 85pp; English.
CC      The sequence comprises the 5' untranslated region, signal sequence,
CC      variable region and part of the constant region for the R6-5-D6
CC      murine Mab light chain. The hybridoma cell line R6-5-D6 producing
CC      the anti ICAM-1 Ab was provided by Boehringer Ingelheim
CC      Pharmaceuticals Inc. The cells were grown and mRNA isolated and
CC      used to prepare cDNA for a library in pSP64 vector DNA. The
CC      library was grown in E. coli HB101 and colonies screened using a
CC      probe complementary to a sequence in the mouse kappa constant
CC      region or with a 980 bp BamHI-EcoRI restriction fragment of a
CC      previously isolated mouse IgG2a constant region clone. Six
CC      positive clones were isolated and rescreened. Positive clones from
CC      the second round of screening were grown and the DNA inserts
CC      sequenced. The DNA was used to construct humanised Abs having
CC      chimeric variable regions, esp. with IgG human constant region
CC      domains. The Abs can be used to treat inflammation, to suppress
CC      metastasis of haematopoietic tumour cells and growth of ICAM-1
CC      expressing tumour cells, to treat viral infection, to suppress
CC      extravascular migration of virally infected leucocytes and to treat
CC      asthma.
CC      See also Q14652 and Q14830.
SQ      Sequence 537 BP: 135 A; 134 C; 128 G; 139 T;

Query Match      72.1%; Score 297.8; DB 1; Length 537;
Best Local Similarity 84.3%; Pred. No. 1.3e-89;
Matches 348; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY      1 ATGAAGTGGCTGTAGGCTGTGGTCTGTGTGTGTGAGTTCCTGTTCCGGAGGT 60
DB      19 ATGAAGTGGCTGTAGGCTGTGGTCTGTGTGTGTGAGTTCCTGTTCCGGAGGT 75
QY      61 GATGTGTGATGACTCAAGTCCACTCTCCCTGCTGTCAACCCCTGGAGAACAGCTTCT 120
DB      76 GATGTGTGATGACTCAAGTCCACTCTCCCTGCTGTCAAGTTCGAGATCAAGCTCC 135
QY      121 ATCTCTTGACAGGTCTAGTCAAGTCTTGCAAGAGTTATGGAAACCTTATTGTCTTG 180
DB      121 ATCTCTTGACAGGTCTAGTCAAGTCTTGCAAGAGTTATGGAAACCTTATTGTCTTG 195
QY      181 TACTGTGAGAAAGCTGGCCAGTCCACAGTCTCTCATCTATGAGATTCCACAGATT 240
DB      181 TACTGTGAGAAAGCTGGCCAGTCCACAGTCTCTCATCTATGAGATTCCACAGATT 255
QY      241 TCTGGGGTGCAGACAGGTTCAAGTGTTCAGGAGACAGATTTCACACTCAAGATC 300
DB      256 TCTGGGGTGCAGACAGGTTCAAGTGTTCAGGAGACAGATTTCACACTCAAGATC 315
QY      301 TCGCGAGTAGAGCTGAGAGCTGGAGTGTATTACTGTCTTACAGGTACATCAACCG 360
DB      316 AGCAGAGTGGAGCTGAGAGTCTGGAGTGTATTACTGTCTTACAGGTACATGTTCT 375

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QY 361 TACAGCTTGGACAGGGGACCAAGTGAATAAAGGGGCTGATCGGCGCC 413
 DB 376 CTCACGCTGGAGGGGAGACCAAGCTGGAATAAAGGGGCTGATCGTCCACC 428

RESULT 7

Q62803 standard; DNA; 394 BP.

AC 062803;
 DE 25-JAN-1995 (first entry)
 DE Immunised murine KC-4 immunoglobulin light chain V-region DN.
 DE Immunoglobulin variable domain; primer: polymerase chain reaction;
 DE murine anti-HMG monoclonal antibody KC-4; human breast carcinoma;
 OS Chimeric Mus musculus.
 OS Chimeric Homo sapiens.

FT Key Location/Qualifiers
 FT cds 1..393

FT mat_peptide /tag= a
 FT /note= "humanised KC-4 VL chain"
 FT 58..393
 FT /tag= b
 FT /product= light-chain-V-region
 FT /note= "humanised framework region"

PD W09411509-A.
 PD 26-MAY-1994.
 PR 16-NOV-1993; U11445.
 PR 16-NOV-1993; US-977696.
 PR 30-SEP-1993; US-129930.
 PR 08-OCT-1993; US-134346.
 PA (CANC-) CANCER RES FUND CONTRA COSTA.
 PI Ceriani RL, Do Couto JFR, Padlan EA, Peterson JA;
 DR P-PSDB: R52822.
 DR P-PSDB: R52822.
 PT New analogue peptide(s) comprising antibody variable regions -
 PT used to develop prods. for use in the detection, diagnosis,
 PT therapy and prevention of neoplasms.
 PS Example 67; Page 90; 109pp; English.
 CC This DNA sequence encodes a humanised murine anti-human carcinoma
 CC antibody light chain variable region. The humanised antibody is
 CC useful for carcinoma therapy and diagnosis and for in vivo imaging
 CC of neoplastic cells. It is also of use in inhibiting the growth of
 CC a primary or metastasised neoplasm.
 SQ Sequence 394 BP; 97 A; 94 C; 98 G; 105 T;

Query Match

Best Local Similarity 71.3%; Score 294.6; DB 1; Length 394;
 Matches 340; Conservative 0; Mismatches 54; Indels 3; Gaps 1;

QY 1 ATGAAGTTCCTGTTAGGCTGTGGTCTTCTGATTCCTGTTCCGGAGGT 60
 DB 1 ATGAAGTTCCTGTTAGGCTGTGGTCTTCTGATTCCTGTTCCGGAGGT 57
 QY 61 GATGTTGATGATCAACCAAGTCCCTGCTGTCACCCCTGGAGAACAGGCTCT 120
 DB 58 GATGTTGATGATCAACCAAGTCCCTGCTGTCACCCCTGGAGAACAGGCTCT 117
 QY 121 ATCTCTTGAGGCTAGTACAGAGTCTTGCACAAAGATTATGGGAACACCTATTGCTTGG 180
 DB 118 ATCTCTTGAGGCTAGTACAGAGTCTTGCACAAAGATTATGGGAACACCTATTGAGATGG 177
 QY 181 TACCTGCAAGAGCTGGGAGCTCCACAGCTCCATCATATGAGGATTTCCAAACATTT 240
 DB 178 TACCTGCAAGAGCTGGGAGCTCCACAGCTCCATCATATGAGGATTTCCAAACATTT 237
 QY 241 TCTGGGGTCCAGACAGGTTCAAGTGTGAGGAGGAGGACAGATTTCACACTCAAGATC 300
 DB 238 TCTGGGGTCCAGACAGGTTCAAGTGTGAGGAGGAGGACAGATTTCACACTCAAGATC 297
 QY 301 TCGCGAGTAGAGGCTGAGGAGCTGGAGTGTATTACTGTTACAGGATACATACGCG 360

DB 298 ACCAGATGAGGAGCTGAGGATGCGGAATTTATCTGTTCAAGGTTACATGTTCCG 357
 QY 361 TACAGCTTGGACAGGGGACCAAGTGAATAAAGGGGCTGATCGGCGCC 397
 DB 358 TACAGCTTGGAGGGGAGACCAAGCTGGAATAAAGGGGCTGATCGTCCACC 394

RESULT 8

Q87533 standard; DNA; 394 BP.

AC 087533;
 DE 27-OCT-1995 (first entry)
 DE Humanised anti-KC-4 antibody VL FR-HZ.
 DE Anti-KC-4 antibody; humanised antibody; cancer; ss.
 OS Synthetic.
 OS Synthetic.

FT Key Location/Qualifiers
 FT cds 1..393
 FT /tag= a

PD W09510776-A.
 PD 20-APR-1995.
 PR 16-NOV-1993; U11444.
 PR 08-OCT-1993; US-134346.
 PA (CANC-) CANCER RESEARCH FUND CONTRA COSTA.
 PI Ceriani RL, Decouto JFR, Peterson JA;
 DR P-PSDB: R70470.
 DR P-PSDB: R70470.
 PT New humanised anti-KC-4 monoclonal antibody - used for detection of
 PT cancer cells, in vivo imaging, ex-vivo purging and treatment of
 PT cancers
 PS Claim 23; Table 21, Page 46; 61pp; English.
 CC Hybridomas were prepd. based on the anti-KC-4 mouse hybridoma ATCC
 CC HB 8710 (US4708930). The murine variable regions were modified at
 CC particular AAs by PCR to provide humanised sequences. The anti-KC-4
 CC humanised DNA sequences for the VH and VL segments are shown in
 CC Q87534 and Q87533 respectively. Plasmid constructions comprising
 CC the humanised variable regions and the human constant regions were
 CC then used to transfect SSp2/0-Ag14 myeloma cells to produce the
 CC humanised anti-KC-4 MAbs. The deduced AA sequences of the
 CC humanised anti-KC-4 variable light and heavy chains are given in
 CC R70470 and R70471 respectively.
 SQ Sequence 394 BP; 97 A; 94 C; 98 G; 105 T;

Query Match

Best Local Similarity 71.3%; Score 294.6; DB 1; Length 394;
 Matches 340; Conservative 0; Mismatches 54; Indels 3; Gaps 1;

QY 1 ATGAAGTTCCTGTTAGGCTGTGGTCTTCTGATTCCTGTTCCGGAGGT 60
 DB 1 ATGAAGTTCCTGTTAGGCTGTGGTCTTCTGATTCCTGTTCCGGAGGT 57
 QY 61 GATGTTGATGATCAACCAAGTCCCTGCTGTCACCCCTGGAGAACAGGCTCT 120
 DB 58 GATGTTGATGATCAACCAAGTCCCTGCTGTCACCCCTGGAGAACAGGCTCT 117
 QY 121 ATCTCTTGAGGCTAGTACAGAGTCTTGCACAAAGATTATGGGAACACCTATTGCTTGG 180
 DB 118 ATCTCTTGAGGCTAGTACAGAGTCTTGCACAAAGATTATGGGAACACCTATTGAGATGG 177
 QY 181 TACCTGCAAGAGCTGGGAGCTCCACAGCTCCATCATATGAGGATTTCCAAACATTT 240
 DB 178 TACCTGCAAGAGCTGGGAGCTCCACAGCTCCATCATATGAGGATTTCCAAACATTT 237
 QY 241 TCTGGGGTCCAGACAGGTTCAAGTGTGAGGAGGAGGACAGATTTCACACTCAAGATC 300
 DB 238 TCTGGGGTCCAGACAGGTTCAAGTGTGAGGAGGAGGACAGATTTCACACTCAAGATC 297
 QY 301 TCGCGAGTAGAGGCTGAGGAGCTGGAGTGTATTACTGTTACAGGATACATACGCG 360
 DB 298 ACCAGATGAGGAGCTGAGGAGTGGGAATTTATCTGTTCAAGGTTACATGTTCCG 357
 QY 361 TACAGCTTGGACAGGGGACCAAGTGAATAAAGGGGCTGATCGGCGCC 397

Db 358 TACACGTTCCGAGGGGAGCCAAAGCTGGAATAAATAC 394

RESULT 9

ID T88870 standard; DNA; 717 BP.

AC T88870;

DT 15-APR-1998 (first entry)

DE L chain subunit of Fas specific antibody coding sequence.

KW Fas; antibody: human; immunoglobulin; variable region; rheumatism;

KW autoimmune disease; rheumatoid arthritis; therapy; CDR; light chain;

KW complementarity determining region; ss.

OS Mus musculus.

Location/Qualifiers

FT Key 1.717

FT sig_peptide 1.57

FT mat_peptide 58.714

FT mat_peptide /tag- b

FT mat_peptide /tag- c

EP-799891-A1.

PD 08-OCT-1997.

PF 27-MAR-1997: 302415.

PR 01-APR-1996: JP-078570.

PA (SANY) SANKYO CO LTD.

PI Ichikawa K, Nakahara K, Serizawa N, Yonehara S;

PI MPI: 97-482673/45.

DR P-PSDB: W31752.

PT Anti-Fas recombinant antibodies - useful for treating auto-immune

PT diseases, especially rheumatoid arthritis

PS Claim 22: Page 34-35; 72pp: English.

CC This sequence represents the coding sequence for the light chain of the

CC protein of the invention. The protein of the invention is a recombinant

CC protein (A), that comprises at least one region corresponding to an

CC immunoglobulin (Ig) variable region which enables the protein to

CC recognise and specifically bind to an antigen, preferably human Fas, and

CC has substantially no more immunogenicity in a human patient than a human

CC antibody. The proteins are useful for treating autoimmune diseases,

CC especially rheumatism (rheumatoid arthritis). (A) is based on a murine

CC monoclonal antibody. As the protein lacks the constant region, it has

CC substantially no more immunogenicity in the human patient than a human

CC antibody.

CC Sequence 717 BP: 194 A: 180 C: 171 G: 172 T:

Query Match 71.3%; Score 294.6; DB 1; Length 717;

Best Local Similarity 83.8%; Pred. No. 1.7e-88;

Matches 346; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 ATGAAGTGGCTGTAGGCTGTGGCTCTCTGTTCTGGATTCTGTTCCGAGGT 60

Db 1 ATGAAGTGGCTGTAGGCTGTGGCTCTCTGTTCTGGATTCTGTTCCGAGGT 57

QY 61 GATGTTGTATGACTCAAAATCCACTCTCCCTGCTGTACACCCCTGAGAACAGCTTC 120

Db 58 GATGTTGTATGACTCAAAATCCACTCTCCCTGCTGTACACCCCTGAGAACAGCTTC 117

QY 121 ATCTCTGAGAGCTGTAGCTAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 180

Db 118 ATCTCTGAGAGCTGTAGCTAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 177

QY 181 TACCTGAGAGCTGTAGCTAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 240

Db 178 TACCTGAGAGCTGTAGCTAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 237

QY 241 TCTGGGGTCCACAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 300

Db 238 TCTGGGGTCCACAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 297

QY 301 TCCGAGTAGAGCTGTAGAGCTGTGGAGTTATTTACTGTTACAAAGTTACACATCAGCG 360

Db 298 AGCAGAGTAGAGCTGTAGAGCTGTGGAGTTATTTACTGTTCTCAAGTTACACATGTTCT 357

QY 361 TACACGTTCCGAGGGGAGCCAAAGCTGGAATAAATAC 413

Db 358 CCGCGCTTCCGAGGGGAGCCAAAGCTGGAATAAATAC 410

RESULT 10

ID V66736 standard; cDNA to mRNA; 717 BP.

AC V66736;

DT 18-JAN-1999 (first entry)

DE Anti-human Fas monoclonal antibody CH11 light chain cDNA.

KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;

KW autoimmune disease; rheumatoid arthritis; therapy; human; mouse;

KW antibody engineering; ds.

OS Synthetic.

OS Mus musculus.

Location/Qualifiers

FT Key 1.57

FT sig_peptide 1.57

FT mat_peptide 58.717

FT mat_peptide /tag- a

FT mat_peptide /tag- b

EP-866131-A2.

PD 23-SEP-1998.

PR 20-MAR-1998: 302113.

PA (SANY) SANKYO CO LTD.

PI Haruyama H, Nakahara K, Serizawa N, Takahashi T,

PI Yonehara S;

PI MPI: 98-482965/42.

DR P-PSDB: W71889.

PT Production of anti-Fas protein humanised antibodies - for use in

PT inducing apoptosis on Fas expressing cells in the treatment of

PT autoimmune diseases, especially rheumatoid arthritis

PS Reference Example 4: Page 61-62; 187pp: English.

CC This cDNA sequence codes for the light chain (see W71889) of

CC mouse anti-human Fas monoclonal antibody CH11. It was obtained

CC from CH11 hybridoma cDNA by PCR amplification (see V6677-78).

CC The heavy chain cDNA in PCR3-L103 is deposited as FERM BP-5428.

CC The invention relates to novel humanised antibodies comprising

CC humanised light and heavy chains (see W71876-81) of CH11. These

CC humanised anti-human Fas antibodies are capable of inducing

CC apoptosis in cells expressing Fas (e.g. synovialocytes) and are

CC useful in the treatment of autoimmune disease and chronic

CC rheumatoid arthritis.

CC Sequence 717 BP: 194 A: 180 C: 171 G: 172 T:

Query Match 71.3%; Score 294.6; DB 1; Length 717;

Best Local Similarity 83.8%; Pred. No. 1.7e-88;

Matches 346; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 ATGAAGTGGCTGTAGGCTGTGGCTCTCTGTTCTGGATTCTGTTCCGAGGT 60

Db 1 ATGAAGTGGCTGTAGGCTGTGGCTCTCTGTTCTGGATTCTGTTCCGAGGT 57

QY 61 GATGTTGTATGACTCAAAATCCACTCTCCCTGCTGTACACCCCTGAGAACAGCTTC 120

Db 58 GATGTTGTATGACTCAAAATCCACTCTCCCTGCTGTACACCCCTGAGAACAGCTTC 117

QY 121 ATCTCTGAGAGCTGTAGCTAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 180

Db 118 ATCTCTGAGAGCTGTAGCTAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 177

QY 181 TACCTGAGAGCTGTAGCTAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 240

Db 178 TACCTGAGAGCTGTAGCTAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 237

QY 241 TCTGGGGTCCACAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 300

Db 238 TCTGGGGTCCACAGAGCTTCAAGAGTTATGGGAACACCTATTGCTTGG 297

QY 301 TCCGAGTAGAGCTGTAGAGCTGTGGAGTTATTTACTGTTACAAAGTTACACATCAGCG 360

Db 298 AGCAGAGTAGAGCTGTAGAGCTGTGGAGTTATTTACTGTTCTCAAGTTACACATGTTCT 357

Db 298 AGCAGAGTGGAGGCTGAGGATCTGGAGTTATTCTGCTCTCAAGTACATGTTCT 357
 QY 361 TACACGTTCCGACAGGGGACCAAGTGAATAAAGCGGCTGATGGCGCC 413
 Db 358 CCGGCGTTCGTTGGAGGACCAACACTGAATCAAGGGGCTGATGCTGCACC 410

RESULT 11

Q14801
 ID Q14801 standard; DNA; 537 BP.

AC Q14801:
 DT 13-FEB-1992 (first entry)
 DE Encodes murine anti-ICAM monoclonal antibody light chain.
 KW Interleukin adhesion molecule; variable region; V(L); mouse;
 KM R6-5-D6 murine MAb; complementarity determining region; CDR; ds.
 OS Mus musculus.

FT Key Location/Qualifiers
 FT CDS 19..537
 FT /tag- a
 FT /product- anti-ICAM_light_chain

PD WO9116927-A.
 PD 14-NOV-1991.
 PF 29-APR-1991; US02942.
 PR 27-APR-1990; GB-009549.
 PA (CELL-) CELTECH LTD.
 PA (BOE) BOEHRINGER INGELHEIM PHA.
 PI Adair JR, Althwal DS, Rothlein RA.
 DR WPI: 91-353533/48.
 DR P-PSDB; R15059.

PT New humanised CDR-grafted anti-ICAM antibodies - used to treat
 PT infections and asthma and in diagnosis
 PS Disclosures: Fig 1; 83pp; English.
 CC The light chain sequence was isolated from a cDNA library prep. from
 CC hybridoma cell line R6-5-D6 which secretes murine IgG2a/kappa
 CC antibody. The library was screened using a probe sequence
 CC complementary to a sequence in mouse kappa constant region. The
 CC murine framework-encoding sequences (i.e. not encoding CDRs) will be
 CC replaced by human framework sequences to produce recombinant (CDR-
 CC grafted humanised) antibody molecules having specificity for ICAM-1.
 SQ Sequence 537 BP; 135 A; 132 C; 129 G; 140 T;

Query Match 70.9%; Score 293; DB 1; Length 537;
 Best Local Similarity 83.5%; Pred. No. 5.2e-88;
 Matches 345; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 ATGAAGTTGCTGTAGGCTGTGCTGCTGTTCTGTTCTGAGATTCCTGTTCCGAGGT 60
 Db 19 ATGAAGTTGCTGTAGGCTGTGCTGCTGTTCTGTTCTGAGATTCCTGTTCCGAGGT 75
 QY 61 GATGTTGATGATCAAGTCCAAAGTCCCTCCCTGCTGATCACTCTTGAGATCAACGCTCT 120
 Db 76 GATGTTGATGATCAAGTCCAAAGTCCCTCCCTGCTGATCACTCTTGAGATCAACGCTCT 135
 QY 121 ATCTCTGCAAGTCTAGTCAAGTCTGTTCAAGAGATTATGGAACACCTATTGTTCTGG 180
 Db 136 ATCTCTGCAAGTCTAGTCAAGTCTGTTCAAGAGATTATGGAACACCTATTGTTCTGG 195
 QY 181 TACCTGCAAGAGCTGCGCAGTCTCCACAGCTCTCATCTATGAGATTTCACACAGATT 240
 Db 196 TACCTGCAAGAGCTGCGCAGTCTCCACAGCTCTCATCTATGAGATTTCACACAGATT 255
 QY 241 TCTGGGGTCCAGACAGGTTCAAGTGGGAGGAGTCAAGGAGATTCACACTCAAGATC 300
 Db 256 TCTGGGGTCCAGACAGGTTCAAGTGGGAGGAGTCAAGGAGATTCACACTCAAGATC 315
 QY 301 TCGGAGTAGAGGCTGAGAGTGGAGTATTACTGCTTACCAAGGTACACATACACCG 360
 Db 316 AGGAGAGTGGAGGCTGAGAGTGGAGTATTACTGCTTACCAAGGTACACATACACCG 375
 QY 361 TACAGTTGGAGGAGGAGTGGAGTGGAGTAAATAAGGGGCTGATGCGGCGC 413

Db 376 CTCACGTTCCGAGGGGAGGACCAAGTGAATAAAGCGGCTGATGCTGCACC 428

RESULT 12

T31332
 ID T31332 standard; cDNA; 447 BP.

AC T31332;
 DT 26-FEB-1997 (first entry)
 DE Anti-idiotype monoclonal antibody 1A7 variable light chain, cDNA.
 KW Murine; mouse; anti-idiotype; monoclonal antibody; MAb; 1A7;
 KM variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
 KM glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
 KM malignant melanoma; soft tissue sarcoma; small cell carcinoma;
 KM vaccine; treatment; palliate; detection; diagnosis;
 KM recombinant production; purification; probe; primer; assay;
 KM amplification; gene therapy; ss.

FT Key Location/Qualifiers
 FT mat_peptide 1..446
 FT /tag- a

PD WO9622373-A2.
 PD 25-JUL-1996.
 PF 17-JAN-1996; US00882.
 PR 17-JAN-1995; US-372676.
 PR 16-JAN-1996; US-372676.
 PA (KENT) UNIV KENTUCKY.
 PI Chatterjee M, Chatterjee SK, Foon KA.
 DR WPI: 96-354530/35.
 DR P-PSDB; W03199.

PT Monoclonal antibody 1A7 and related polynucleotide(s) and
 PT polypeptide(s) - useful to treat or palliate a GD2-associated
 PT disease, e.g. melanoma and glioma
 PS Claim 10; Fig 1; 141pp; English.
 CC The present sequence encodes the murine anti-idiotype monoclonal
 CC antibody (MAb) 1A7 variable light chain. MAb 1A7 was raised against
 CC the anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
 CC or palliate such diseases. They can also be used in a vaccine to treat
 CC risk of recurrence of a clinically detectable tumour, and detect an
 CC anti-GD2 Ab bound to a tumour cell.
 CC MAb 1A7 overcomes immune tolerance and induces an immune response
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and
 CC GD2-specific cells (cellular response). It can be used to purify
 CC anti-1A7 (Ab3), anti-GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or
 CC anti-GD2 activity.
 CC The cDNA can be used in expression systems for 1A7 prodn., and in
 CC the prepn. of probes and primers to respectively assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.
 SQ Sequence 447 BP; 106 A; 110 C; 108 G; 123 T;

Query Match 70.9%; Score 293; DB 1; Length 447;
 Best Local Similarity 83.5%; Pred. No. 4.8e-88;
 Matches 345; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 ATGAAGTTGCTGTAGGCTGTGCTGCTGTTCTGTTCTGAGATTCCTGTTCCGAGGT 60
 Db 1 ATGAAGTTGCTGTAGGCTGTGCTGCTGTTCTGTTCTGAGATTCCTGTTCCGAGGT 57
 QY 61 GATGTTGATGATCAAGTCCAAAGTCCCTCCCTGCTGATCACTCTTGAGATCAACGCTCT 120
 Db 58 GATGTTGATGATCAAGTCCAAAGTCCCTCCCTGCTGATCACTCTTGAGATCAACGCTCT 117
 QY 121 ATCTCTGCAAGTCTAGTCAAGTCTGTTCAAGAGATTATGGAACACCTATTGTTCTGG 180
 Db 118 ATCTCTGCAAGTCTAGTCAAGTCTGTTCAAGAGATTATGGAACACCTATTGTTCTGG 177
 QY 181 TACCTGCAAGAGCTGCGCAGTCTCCACAGCTCTCATCTATGAGATTTCACACAGATT 240

Db 178 TACCTACGAAACAGGCCAGCTCTCCAAACCTCGATCTACTTGTTCACACCGATT 237
Qy 241 TCTGGGGTCCAGACAGCTTCACTGCTGCTTCAAGGACAGATTTCACACTCAAGATC 300
Db 238 TCTGGGGTCCAGACAGCTTCACTGCTGCTTCAAGGACAGATTTCACACTCAAGATC 297
Qy 301 TCGGAGTAGAGGCTGAGGAGCTGATTAATCTCTTACCAAGATACATCAGCCG 360
Db 298 AGCAGAGTAGAGGCTGAGGAGCTGATTAATCTCTTACCAAGATACATCAGCCG 357
Qy 361 TACACGTTCCGACAGGGGACCAAGTGAATTAACAGCGCTGATGCGGCCG 413
Db 358 TGGAGCTTCGGTGGAGGACCAAGCTGGAATCAACAGCGCTGATGCGGCCG 410

RESULT 13

062790
ID 062790 standard; DNA: 394 BP.
AC 062790;
DT 24-JAN-1995 (first entry)
DE Humanised murine Bre3 immunoglobulin light chain V-region DNA.
KW Immunoglobulin variable domain; primer: polymerase chain reaction;
KW chimeric antibody; human mammary fat globule; human breast carcinoma;
KW murine anti-HMFg monoclonal antibody Bre3; humanised analogue; ss.
OS Chimeric Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..393
FT /tag= a
FT /note= "humanised Bre3 VL chain"
FT /tag= b
FT /product= light_chain_V-region
FT /note= "humanised framework region"

PN W09411508-A.
PD 26-MAY-1994.
PE 16-NOV-1993; U11445.
PR 16-NOV-1992; US-977696.
PR 30-SEP-1993; US-129930.
PR 08-OCT-1993; US-134346.
PA (CANC-) CANCER RES FUND CONTRA COSTA.
PI Certani RL, DO Couto FJR, Padian EA, Peterson JA;
DR WPI: 94-183510/22.
DR P-PSDB: R52806.
PT New analogue peptide(s) comprising antibody variable regions -
PT used to develop prods. for use in the detection, diagnosis,
PT therapy and prevention of neoplasms
PS Claim 32; Page 81; 109pp; English.
CC This DNA sequence encodes a preferred analogue peptide which
CC selectively binds to an antigen on the surface or in the cytoplasm
CC of a neoplastic cell. The peptide comprises at least one CDR and at
CC least one V region of L- or H-chain from an anti-human mammary fat
CC globule antigen antibody (i.e. murine Bre3 antibody) but where 1 to
CC 46 amino acids in the FRs are substituted by their homologues from
CC human antibodies (humanised). The humanised antibody is useful for
CC carcinoma therapy and diagnosis and for in vivo imaging of
CC neoplastic cells. It is also of use in inhibiting the growth of a
CC primary or metastasised neoplasm.
SQ Sequence 394 BP; 89 A; 95 C; 99 G; 111 T;

Query Match 70.6%; Score 291.4; DB 1; Length 394;
Best Local Similarity 85.1%; Pred. No. 1.5e-87;
Matches 338; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

Qy 1 ATGAAGTTGCTGTAGGCTGTGCTGCTTGTGTTCTGGATTCCTGTTCCGAGGT 60
Db 1 ATGAAGTTGCTGTAGGCTGTGCTGCTTGTGTTCTGGATTCCTGTTCCGAGGT 57
Qy 61 GATGTGTGATGATCAAAAGTCCACTCTCCCTGCTGTCACCCCGGAGAACGCTTCT 120
Db 58 GATGTGTGATGATCAAAAGTCCACTCTCCCTGCTGTCACCCCGGAGAACGCTTCT 117

Qy 121 ATCTCTGACAGTCTAGTCAGAGTCTTGCAAGAGATTATGGGAACACCTATTGTCTGG 180
Db 118 ATCTCTGACAGTCTAGTCAGAGTCTTGCAAGAGATTATGGGAACACCTATTGTCTGG 177
Qy 181 TACCTGCAAGAGCTTGGCCAGTCTTCACAGTCTCTCATCTATGGGATTTCACAGATT 240
Db 178 TTCTGTGAGAGCCAGGACCTGCTCCAAAGCTCTGATTTATAGGGTTCATCCGATT 237
Qy 241 TCTGGGGTCCAGACAGCTTCACTGCTGCTTCAAGGACAGATTTCACACTCAAGATC 300
Db 238 TCTGGGGTCCAGACAGCTTCACTGCTGCTTCAAGGACAGATTTCACACTCAAGATC 297
Qy 301 TCGGAGTAGAGGCTGAGGAGCTGATTAATCTCTTACCAAGATACATCAGCCG 360
Db 298 AGCAGAGTAGAGGCTGAGGAGCTGATTAATCTCTTACCAAGATACATCAGCCG 357
Qy 361 TACACGTTCCGACAGGGGACCAAGTGAATTAAC 397
Db 358 TGGAGCTTCGGTGGAGGACCAAGCTGGAATCAAC 394

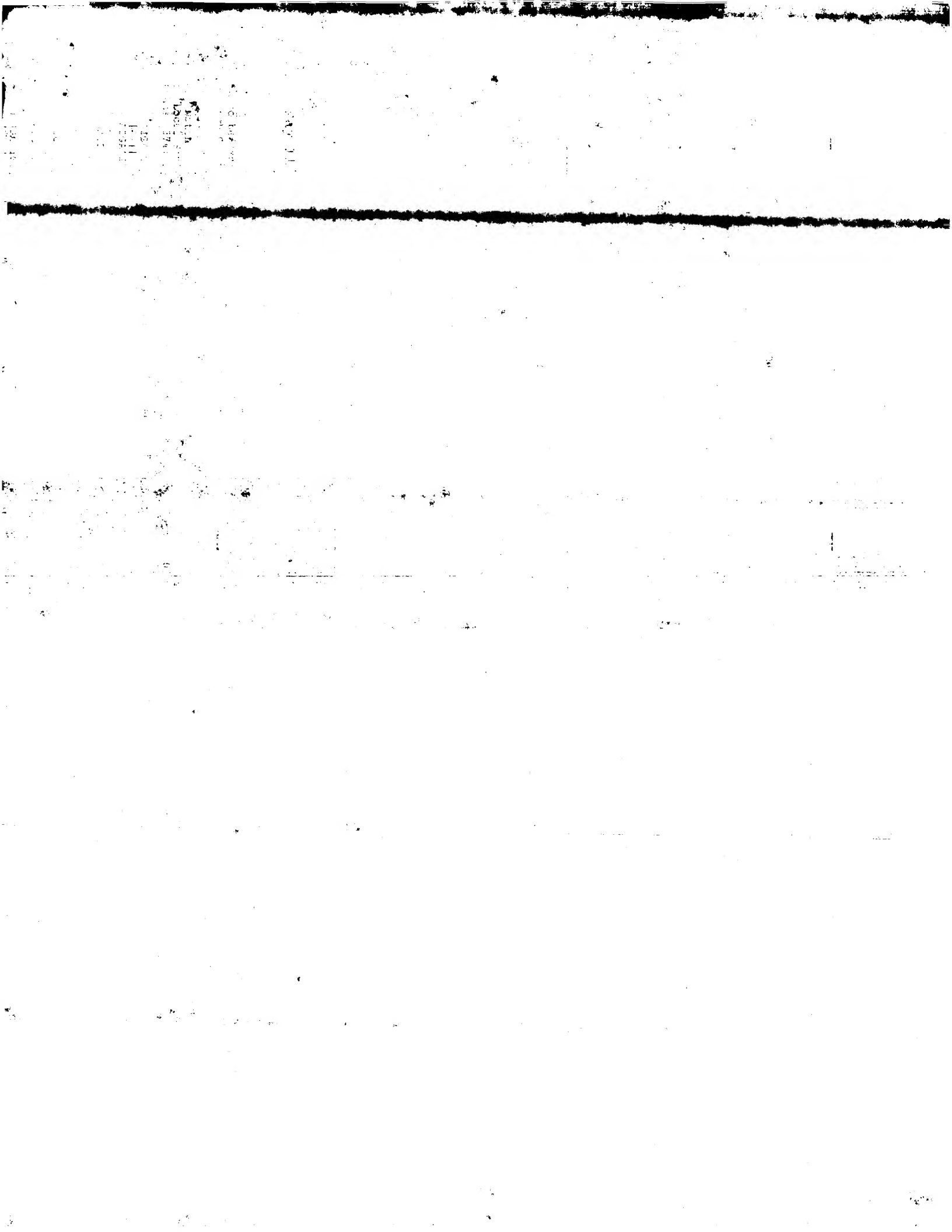
RESULT 14

062763
ID 062763 standard; cDNA: 394 BP.
AC 062763;
DT 24-JAN-1995 (first entry)
DE Murine KC-4 immunoglobulin light chain variable region cDNA.
KW Immunoglobulin variable domain; primer: polymerase chain reaction;
KW chimeric antibody; human milk fat globule; human breast carcinoma;
KW murine anti-human carcinoma monoclonal antibody KC-4; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT cds 1..393
FT /tag= a
FT /note= "KC-4 VL chain (no termination codon)"
FT /tag= b
FT /product= light_chain_V-region

PN W09411508-A.
PD 26-MAY-1994.
PE 15-NOV-1993; U11316.
PR 13-NOV-1992; US-977706.
PR 13-NOV-1992; US-977706.
PR 28-SEP-1993; US-128015.
PA (CANC-) CANCER RES FUND CONTRA COSTA.
PI WPI: 94-183509/22.
DR P-PSDB: R52772.
PT Chimeric human-murine polypeptide(s) specific for human mammary
PT fat globule antigen - for imaging, diagnosing and treating
PT neoplasia, with less undesirable immunogenic response
PS Example 26; Page 40; 54pp; English.
CC An initial isolation of cDNAs coding for murine anti-human breast
CC carcinoma MAb KC-4 was performed using PCR with commercially
CC available primers (see 062751-062758, available from NOVAGEN).
CC Subsequent cloning using PCR primers J020, J021, J022 and J024
CC (see 062759-062762) resulted in the isolation of the mouse Ig
CC variable domains. The amplified cDNAs were sequenced (062763 and
CC 062764). Chimeric mouse-human antibodies were constructed
CC using human constant regions so as to produce less immunogenic
CC polypeptides which retained the anti-human carcinoma binding
CC specificity of KC-4.
SQ Sequence 394 BP; 98 A; 91 C; 96 G; 109 T;

Query Match 69.4%; Score 286.6; DB 1; Length 394;
Best Local Similarity 84.4%; Pred. No. 6.1e-86;
Matches 335; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

Qy 1 ATGAAGTTGCTGTAGGCTGTGCTGCTTGTGTTCTGGATTCCTGTTCCGAGGT 60
Db 1 ATGAAGTTGCTGTAGGCTGTGCTGCTTGTGTTCTGGATTCCTGTTCCGAGGT 57
Qy 61 GATGTGTGATGATCAAAAGTCCACTCTCCCTGCTGTCACCCCGGAGAACGCTTCT 120




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DB      1  MRLPAQLLMLMWPVGSSGDVMTQSPSLPTLPGPASPISCRSSQSLVSDGNTHLW 60
QY      61  YLQKPGQSPQLLYIGISNRFSGVDPDRFSGSGSTDTLTKISRVEADGVYVYCLQGTROP 120
DB      61  FQORPGQSPRLILYKYNRDSGVPDRFSGSGSTDTLTKISRVEADGVYVYCMQGTTHW 120
QY      121  YTFGGGTKEIKR 133
DB      121  YTFGGGTKEIKR 133

RESULT  3
B32513
Ig kappa chain precursor V region (MRL4) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 20-Mar-1998
C:Accession: B32513
R:Kofler, R.; Strichal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94689; MUID:88331394
A:Accession: B32513
A:Molecule type: DNA
A:Residues: 1-131 <KOF>
A:Cross-references: GB:M20828; NID:9196937; PID:9196938
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

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Query Match      77.2%; Score 555.5; DB 2; Length 131;
Best Local Similarity 81.8%; Pred. No. 3.2e-43;
Matches 108; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

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QY      1  MRLPYRLVLLFLFWIPVSGDVMTQSPSLPTPEGPASISCRSSQSLAKSYGNTYLSW 60
      1  MRLPYRLVLLFLFWIPVSGDVMTQSPSLPTPEGPASISCRSSQSLAKSYGNTYLSW 59
DB      61  YLQKPGQSPQLLYIGISNRFSGVDPDRFSGSGSTDTLTKISRVEADGVYVYCLQGTROP 120
      60  YLQKPGQSPRLILYKYNRDSGVPDRFSGSGSTDTLTKISRVEADGVYVYCMQGTTHW 119
QY      121  YTFGGGTKEIKR 132
      121  YTFGGGTKEIKR 131
DB      120  YTFGGGTKEIKR 131

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RESULT  4
K2HURP
Ig kappa chain precursor V-II region (RPM1) - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997
C:Accession: A01890
R:Klobeck, H.G.; Meindl, A.; Combrat, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6439-6513, 1985
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A:Reference number: A93588; MUID:86041852
A:Accession: A01890
A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A>Note: The sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPM1) #status predicted <MAT>
F:21-43/Region: framework 1

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F:36-115/Domain: Immunoglobulin homology <IMN>
F:44-59/Region: complementarity-determining 1
F:60-74/Region: framework 2
F:75-81/Region: complementarity-determining 2
F:82-113/Region: framework 3
F:114-122/Region: complementarity-determining 3
F:123-133/Region: framework 4
F:43-113/Disulfide bonds: #status predicted

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Query Match      77.1%; Score 555; DB 1; Length 133;
Best Local Similarity 79.7%; Pred. No. 3.6e-43;
Matches 106; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

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QY      1  MRLPYRLVLLFLFWIPVSGDVMTQSPSLPTPEGPASISCRSSQSLAKSYGNTYLSW 60
DB      1  MRLPAQLLMLMWPVGSSGDVMTQSPSLPTLPGPASPISCRSSQSLVSDGNTHLW 60
QY      61  YLQKPGQSPQLLYIGISNRFSGVDPDRFSGSGSTDTLTKISRVEADGVYVYCLQGTROP 120
DB      61  FQORPGQSPRLILYKYNRDSGVPDRFSGSGSTDTLTKISRVEADGVYVYCMQGTTHW 120
QY      121  YTFGGGTKEIKR 133
DB      121  YTFGGGTKEIKR 133

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RESULT 5

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B30577
Ig kappa chain precursor V region (MRL10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
C:Accession: B30577
R:Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Th
J. Exp. Med. 161, 805-815, 1985
A:Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r
A:Reference number: A30577; MUID:85159423
A:Accession: B30577
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <KOF>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

```

```

Query Match      76.9%; Score 553.5; DB 2; Length 131;
Best Local Similarity 81.1%; Pred. No. 4.8e-43;
Matches 107; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

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```

QY      1  MRLPYRLVLLFLFWIPVSGDVMTQSPSLPTPEGPASISCRSSQSLAKSYGNTYLSW 60
DB      1  MRLPYRLVLLFLFWIPVSGDVMTQSPSLPTPEGPASISCRSSQSLAKSYGNTYLSW 59
QY      61  YLQKPGQSPQLLYIGISNRFSGVDPDRFSGSGSTDTLTKISRVEADGVYVYCLQGTROP 120
DB      60  YLQKPGQSPRLILYKYNRDSGVPDRFSGSGSTDTLTKISRVEADGVYVYCMQGTTHW 119
QY      121  YTFGGGTKEIKR 132
DB      120  YTFGGGTKEIKR 131

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RESULT 6

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B25912
Ig kappa chain precursor V region (W3129) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Mar-1998
C:Accession: B25912
R:Borden, P.; Kabat, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443, 1987
A:Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and light
A:Reference number: A94147; MUID:87175689
A:Accession: B25912

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[illegible]

RL NATURE 309:73-76(1984).
 DR EMBL; 200009; -; NOT_ANNOTATED_CDS.
 DR PIR; A01889; K2HUGM.
 DR HSSP; P01679; ICBV.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT NON_TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION (GM607).
 FT DOMAIN 5 27 FRAMEWORK 1.
 FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 44 58 FRAMEWORK 2.
 FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 66 97 FRAMEWORK 3.
 FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 107 116 FRAMEWORK 4.
 FT DISULFID 27 97 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12664 MW; E09E9ACC CRC32;

Query Match 69.6%; Score 501; DB 1; Length 117;
 Best Local Similarity 85.3%; Pred. No. 8.8e-42;
 Matches 99; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

QY 18 SGGDVVTGSPSLPYTPGEPASISCRSSQSLAKSYGNTYLSWYLOKPGQSPOLLITIGIS 77
 DB 2 SSQDIWVTGSPSLPYTPGEPASISCRSSQSLHSDGFDYLNWYLOKPGQSPOLLITIGIS 61
 QY 78 NRPFGVDRFGSGSGTDFTLKISRVEAEDVGVYICLOGTHOPYTFGQGTVEIKR 133
 DB 62 NRASGVDRFGSGSGTDFTLKISRVEAEDVGVYICMGLQTPOTFGQGTVEIKR 117

RESULT 3
 KY2D_HUMAN STANDARD; PRT; 113 AA.
 AC P01617;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (TEW).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE (BENCE-JONES PROTEIN TEW).
 RX MEDLINE: 74148480.
 RA PUTNAM F.W., WHITLEY E.J. JR., PAUL C., DAVIDSON J.N.;
 RL BIOCHEMISTRY 12:3763-3780(1973).
 RN [2]
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
 RX MEDLINE: 73166638.
 RA TERRY W.D., PAGE D.L., KIMURA S., ISOBE T., OSSEMAN E.F.,
 RA GLENNER G.G.;
 RL J. CLIN. INVEST. 52:1276-1281(1973).
 CC -1- THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE
 CC JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
 CC -1- THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH
 CC PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 DR PIR; A01888; K2HUTW.
 DR HSSP; P01679; ICBV.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; AMYLOID.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 40 54 FRAMEWORK 2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 62 93 FRAMEWORK 3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12316 MW; FC2B2819 CRC32;

Query Match 68.2%; Score 491; DB 1; Length 113;
 Best Local Similarity 82.3%; Pred. No. 7.8e-41;
 Matches 93; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 21 DVVMTGSPSLPYTPGEPASISCRSSQSLAKSYGNTYLSWYLOKPGQSPOLLITIGISNR 80
 DB 1 DIWMTGSPSLPYTPGEPASISCRSSQSLHSDGFDYLNWYLOKPGQSPOLLITIGISNR 60
 QY 81 SGVDRFGSGSGTDFTLKISRVEAEDVGVYICLOGTHOPYTFGQGTVEIKR 133
 DB 61 SGVDRFGSGSGTDFTLKISRVEAEDVGVYICMGLQTPOTFGQGTVEIKR 113

RESULT 4
 KY2A_HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (CDW).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 68242259.
 RA HITSCHMANN N.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 348:1718-1722(1967).
 RN [2]
 RP REVISIONS TO 50; 52; 96 AND 97.
 RX MEDLINE: 70063440.
 RA HITSCHMANN N.;
 RL NATURWISSENSCHAFTEN 56:195-205(1969).
 CC -1- THIS IS A BENCE-JONES PROTEIN.
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC CC
 DR PIR; A01885; K2HUCM.
 DR HSSP; P01607; IIGI.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DISULFID 24 95 BY SIMILARITY.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12676 MW; 5500220A CRC32;

Query Match 66.6%; Score 479.5; DB 1; Length 115;
 Best Local Similarity 82.5%; Pred. No. 1e-39;
 Matches 94; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

QY 21 DVVMTGSPSLPYTPGEPASISCRSSQSLAKS-YGNTYLSWYLOKPGQSPOLLITIGISNR 79
 DB 2 DIWMTGSPSLPYTPGEPASISCRSSQSLHSDGFDYLNWYLOKPGQSPOLLITIGISNR 61
 QY 80 FSGVDRFGSGSGTDFTLKISRVEAEDVGVYICLOGTHOPYTFGQGTVEIKR 133
 DB 62 ASGVDRFGSGSGTDFTLKISRVEAEDVGVYICMGLQTPOTFGQGTVEIKR 115

RESULT 5
 KY2G_MOUSE STANDARD; PRT; 113 AA.
 AC P01631;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (26-10).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;

RX MEDLINE; 83178921.
RA NOVOTNY J., MARGOLIES M.N.;
RL BIOCHEMISTRY 22:1153-1158(1983).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT
CC BINDS DIGOXIN.
DR PIR; A01914; KWS26.
DR HSP; P01607; 11GI.
KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY; HYBRIDOMA.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 24 39 FRAMEWORK 2.
FT DOMAIN 3 40 54 FRAMEWORK 3.
FT DOMAIN 4 55 61 FRAMEWORK 4.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 103 112 FRAMEWORK 4.
FT NON_TER 23 93 BY SIMILARITY.
SQ SEQUENCE 113 AA; 12273 MW; 58372CBE CRC32;

Query Match 65.7%; Score 473; DB 1; Length 113;
Best Local Similarity 80.5%; Pred. No. 4.2e-39;
Matches 91; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

OY 21 DVVATQSPSLPYTPGEPASISCRSSQSLAKSYNTYLSWYLRQPGSPOLLITIGISNRF 80
DB 1 DVVATQSPSLPYTPGEPASISCRSSQSLAKSYNTYLSWYLRQPGSPOLLITIGISNRF 60
OY 81 SGVDFRSGSGSGTDFTLKISRVAEDVGYCCLOGTHOPTFGQGTVEIKR 133
DB 61 SGVDFRSGSGSGTDFTLKISRVAEDVGYCCLOGTHOPTFGQGTVEIKR 113

RESULT 6
KV2L_HUMAN STANDARD; PRT; 113 AA.
ID P01615;
AC 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-II REGION (FR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP MEDLINE; 76253627.
RA RIESEN W.F., JATON J.-C.;
RL BIOCHEMISTRY 15:3829-3833(1976).
CC -1- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUR.
DR HSP; P01607; 1LEL.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 24 39 FRAMEWORK 2.
FT DOMAIN 3 40 54 FRAMEWORK 3.
FT DOMAIN 4 55 61 FRAMEWORK 4.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 103 112 FRAMEWORK 4.
FT NON_TER 23 93 BY SIMILARITY.
SQ SEQUENCE 113 AA; 12660 MW; 53CADDE CRC32;

Query Match 64.7%; Score 466; DB 1; Length 113;
Best Local Similarity 79.6%; Pred. No. 2e-38;
Matches 90; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

OY 21 DVVATQSPSLPYTPGEPASISCRSSQSLAKSYNTYLSWYLRQPGSPOLLITIGISNRF 80
DB 1 DVVATQSPSLPYTPGEPASISCRSSQSLAKSYNTYLSWYLRQPGSPOLLITIGISNRF 60

OY 81 SGVDFRSGSGSGTDFTLKISRVAEDVGYCCLOGTHOPTFGQGTVEIKR 133
DB 61 SGVDFRSGSGSGTDFTLKISRVAEDVGYCCLOGTHOPTFGQGTVEIKR 113

RESULT 7
KV2C_HUMAN STANDARD; PRT; 112 AA.
ID P01616;
AC 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-II REGION (MIL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP DREYER W.J., GRAY W.R., HOOD L.E.;
RA COLD SPRING HARB. SYMP. QUANT. BIOL. 32:353-367(1967).
RL -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- THIS IS A BENGE-JONES PROTEIN.
DR PIR; A01887; K2HML.
DR HSP; P01679; 1CBV.
KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 24 38 FRAMEWORK 2.
FT DOMAIN 3 39 53 FRAMEWORK 3.
FT DOMAIN 4 54 60 FRAMEWORK 4.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 102 111 FRAMEWORK 4.
FT NON_TER 23 92 BY SIMILARITY.
SQ SEQUENCE 112 AA; 12055 MW; C487DFDF CRC32;

Query Match 63.0%; Score 453.5; DB 1; Length 112;
Best Local Similarity 75.2%; Pred. No. 3.2e-37;
Matches 85; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

OY 21 DVVATQSPSLPYTPGEPASISCRSSQSLAKSYNTYLSWYLRQPGSPOLLITIGISNRF 80
DB 1 DVVATQSPSLPYTPGEPASISCRSSQSLAKSYNTYLSWYLRQPGSPOLLITIGISNRF 59
OY 81 SGVDFRSGSGSGTDFTLKISRVAEDVGYCCLOGTHOPTFGQGTVEIKR 133
DB 60 SGVDFRSGSGSGTDFTLKISRVAEDVGYCCLOGTHOPTFGQGTVEIKR 112

RESULT 8
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID P18135;
AC 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HAB).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
RL J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; P10022; K3HUA.
DR HSP; P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HAI).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON TER 129
 SO SEQUENCE 129 AA: 14073 MW: 2C44B85E CRC32;

Query Match 61.1%; Score 440; DB 1; Length 129;
 Best Local Similarity 63.2%; Pred. No. 7.4e-36;
 Matches 84; Conservative 22; Mismatches 23; Indels 4; Gaps 1;

OY 1 MKLPVRLVLLFWIPVSGDVMTQSPILSPVTPGEPASISCRSSQSLAKSYGNTYLSW 60
 DB 1 METPAQLFLLLMLPDTGTEIVLTQSPGTLSPGERATLISCRASQSVSSS----YLAW 56
 OY 61 YLQKRGSPOLLIGISNRFSGVDPDRFSGSGGTDFLTLSRVEADYGVYCCLOGTHQP 120
 DB 57 YQKRGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTLSRLEPDAVYVYCCQYGTSP 116
 OY 121 YTFGGGTVEIKR 133
 DB 117 RTFGGGRVEIKR 129

RESULT 9
 ID KV3M_HUMAN STANDARD: PRT: 129 AA.
 AC P18136:
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (HIC).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88171307.
 RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
 RL J. EXP. MED. 167:840-852(1988).
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 CC PIR: P10021; K3HUI.
 DR HSSP; P01607; IDPB.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON TER 129
 SO SEQUENCE 129 AA: 14070 MW: DD00C369 CRC32;

Query Match 61.0%; Score 439; DB 1; Length 129;
 Best Local Similarity 62.4%; Pred. No. 9.3e-36;
 Matches 83; Conservative 23; Mismatches 23; Indels 4; Gaps 1;
 OY 1 MKLPVRLVLLFWIPVSGDVMTQSPILSPVTPGEPASISCRSSQSLAKSYGNTYLSW 60
 DB 1 METPAQLFLLLMLPDTGTEIVLTQSPGTLSPGERATLISCRASQSVSSS----YLAW 56

DB 1 METPAQLFLLLMLPDTGTEIVLTQSPGTLSPGERATLISCRASQSVSSS----YLAW 56
 OY 61 YLQKRGSPOLLIGISNRFSGVDPDRFSGSGGTDFLTLSRVEADYGVYCCLOGTHQP 120
 DB 57 YQKRGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTLSRLEPDAVYVYCCQYGTSP 116
 OY 121 YTFGGGTVEIKR 133
 DB 117 RTFGGGRVEIKR 129

RESULT 10
 ID KV2E_MOUSE STANDARD: PRT: 113 AA.
 AC P01630:
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (7S34.1).
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 83256427.
 RA CHANG J.-Y., HERBST H., AEBERSOLD R., BRAUN D.G.;
 RL BIOCHEM. J. 211:173-180(1983).
 CC -1- THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL ANTIBODY
 AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
 DR PIR: A01913; KMS75.
 DR HSSP; P01679; ICGS.
 KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY; HYBRIDOMA.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 40 54 FRAMEWORK 2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 62 93 FRAMEWORK 3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON TER 113
 SO SEQUENCE 113 AA: 12496 MW: AE067DC8 CRC32;

Query Match 59.4%; Score 428; DB 1; Length 113;
 Best Local Similarity 74.3%; Pred. No. 9.1e-35;
 Matches 84; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

OY 21 DVMTQSPILSPVTPGEPASISCRSSQSLAKSYGNTYLSWYLQKRGSPOLLIGISNRF 80
 DB 1 DIVMTQSPILSPVTPGEPASISCRSSQSLAKSYGNTYLSWYLQKRGSPOLLIGISNRF 80
 OY 81 SGVDPDRFSGSGGTDFLTLSRVEADYGVYCCLOGTHQPDTFGGTVEIKR 133
 DB 61 SGVDPDRFSGSGGTDFLTLSRVEADYGVYCCLOGTHQPDTFGGTVEIKR 113

RESULT 11
 ID KV2E_MOUSE STANDARD: PRT: 113 AA.
 AC P03976:
 DT 23-OCT-1986 (REL. 02, CREATED)
 DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (17S29.1).
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 85128968.
 RA AEBERSOLD R., HERBST H., GRUTTER T., CHANG J.Y., BRAUN D.G.;

RL HOPE-SEYLER'S 2. PHYSIOL. CHEM. 365:1375-1383(1984).
 CC -1- ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
 DR PIR; A01912; KMS17.
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 24 39 FRAMEWORK 2.
 FT DOMAIN 3 40 54 FRAMEWORK 3.
 FT DOMAIN 4 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 62 93 FRAMEWORK 3.
 FT DOMAIN 6 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 103 112 FRAMEWORK 4.
 FT NON_TER 23 93 BY SIMILARITY.
 SQ SEQUENCE 113 AA; 12390 MW; 6A4552AE CRC32;

Query Match 58.6%; Score 422; DB 1; Length 113;
 Best Local Similarity 74.3%; Pred. No. 3.5e-34;
 Matches 84; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

Oy 21 DVMATQSPLEPTGEPASISCRSSQSLAKSYGNTYLSMYLQKPGSPOLLIGISNRF 80
 Db 1 DIVMTQAFNSNPTVLTGTSASISCRSSKSLHNGITLYLWYLOKRGSPOLLIGMSNLA 60
 Oy 81 SGVDPFSGSGSGDTFTLKISRVEADVGVYCCLOGTHQPTFGGTKEIKR 133
 Db 61 SGVDPFSGSGSGDTFTLKISRVEADVGVYCCANLHLPYFGGTKEIKR 113

RESULT 12
 KV2D_MOUSE STANDARD; PRT; 112 AA.
 ID KV2D_MOUSE
 AC P01629;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (251.33).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 83055101.
 RA HOPE-BEST H., CHANG J.Y., AEBERSOLD R., BRAUN D.G.;
 RL HOPE-SEYLER'S 2. PHYSIOL. CHEM. 363:1069-1076(1982).
 CC -1- THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL ANTIBODY
 CC AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
 DR PIR; A01911; KMS1.
 KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 24 39 FRAMEWORK 2.
 FT DOMAIN 3 40 54 FRAMEWORK 3.
 FT DOMAIN 4 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 62 93 FRAMEWORK 3.
 FT DOMAIN 6 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 103 112 FRAMEWORK 4.
 FT NON_TER 23 93 BY SIMILARITY.
 SQ SEQUENCE 112 AA; 12221 MW; C16DB265 CRC32;

Query Match 58.3%; Score 420; DB 1; Length 112;
 Best Local Similarity 75.0%; Pred. No. 5.3e-34;
 Matches 84; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Oy 21 DVMATQSPLEPTGEPASISCRSSQSLAKSYGNTYLSMYLQKPGSPOLLIGISNRF 80
 Db 1 DIVMTQAFNSNPTVLTGTSASISCRSSKSLHNGITLYLWYLOKRGSPOLLIGMSNLA 60
 Oy 81 SGVDPFSGSGSGDTFTLKISRVEADVGVYCCLOGTHQPTFGGTKEIKR 132

Db 61 SGVDPFSGSGSGDTFTLKISRVEADVGVYCCANLHLPYFGGTKEIKR 112

RESULT 13
 KV4C_HUMAN STANDARD; PRT; 134 AA.
 ID KV4C_HUMAN
 AC P06314;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (B17).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86041854.
 RA MARSH P., MILLS F., GOULD H.;
 RL NUCLEIC ACIDS RES. 13:6531-6544(1985).
 RN [2]
 RP REVISION TO 76.

RA SUBMITTED (OCT-1986) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; X02890; G37910;
 DR PIR; A01905; K4H017.
 DR HSSP; P01607; 21MN.

KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-III REGION (B17).
 FT DOMAIN 1 21 43 FRAMEWORK 1.
 FT DOMAIN 2 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 61 75 FRAMEWORK 2.
 FT DOMAIN 4 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 83 114 FRAMEWORK 3.
 FT DOMAIN 6 115 121 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 122 133 FRAMEWORK 4.
 FT NON_TER 43 114 BY SIMILARITY.
 SQ SEQUENCE 134 AA; 14966 MW; BB63E06A CRC32;

Query Match 58.3%; Score 419.5; DB 1; Length 134;
 Best Local Similarity 64.2%; Pred. No. 7.3e-34;
 Matches 86; Conservative 16; Mismatches 31; Indels 1; Gaps 1;

Oy 1 MKLPRLVLLFWTPGSGGVNMQSPLEPTGEPASISCRSSQSLAKSYGNTYLS 59
 Db 1 MYLQTVFTSLTLWTSGAVGDIWMTQSPSLAVSLGERATTNCKSSOSILYSSDKRYLA 60
 Oy 60 WYLKRGSPOLLIGISNRFSGVDPDRFSGSGSGDTFTLKISRVEADVGVYCCLOGTHQ 119
 Db 61 WYQKRGSPOLLIGISNRFSGVDPDRFSGSGSGDTFTLTSSQAEADVAYTCQGYNL 120
 Oy 120 PYTFGSGTKEIKR 133
 Db 121 PYTFGSGTKEIKR 134

RESULT 14
 KV3H_HUMAN STANDARD; PRT; 129 AA.
 ID KV3H_HUMAN
 AC P04207;
 DT 20-MAR-1987 (REL. 04, CREATED)
 DT 01-NOV-1980 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (CLL) (RHEUMATOID FACTOR).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86177570.
 RA JIRIK F.R., SORGE J., FONG S., HEITZMANN J.G., CURD J.G., CHEN P.P.,

RA GOLDSTEIN R., CARSON D.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:2195-2199(1986).
DR EMBL: M12740; G553486; -
DR PIR: A01898; K3HCL.
DR HSSP: P01607; 1AKG.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 1 129 IG KAPPA CHAIN V-III REGION (CLL).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 2F344868 CRC32;

Query Match Best Local Similarity 57.9%; Score 417; DB 1; Length 129;
Matches 80; Conservative 24; Mismatches 24; Indels 6; Gaps 2;

OY 1 MKLPVRLVLLFWIPVSGDVMTQSPVLPVTPGEPASISCRSSQSLAKSYGNTYLSW 60
DB 1 MEAPQQLFLLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSN-----LAW 55
OY 61 YLQKPGQSPQLLYIGISNRFSGVPDRFSGSGGTDFTLKISRVEADGVVYCCLOGTHQ 119
DB 56 YQKRGQSPRLIRDPASSRANGIPDRFSGSGGTDFTLKISRLEPEDPAVYCCQYSTSP 115
OY 120 PYFGGQTVETIKR 133
DB 116 PWTFGGTVETIKR 129

RESULT 15
KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86041852.
RA KLOBECK H.G., MEINDL A., COMBRIATO G., SOLOMON A., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
DR EMBL: Z00021; G33179; -
DR PIR: A01899; K3H041.
DR HSSP: P01607; 3HEM.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 1 128 IG KAPPA CHAIN V-III REGION (IARC/BL41).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; 318E08AF CRC32;

Query Match Best Local Similarity 57.7%; Score 415.5; DB 1; Length 128;
Matches 80; Conservative 24; Mismatches 24; Indels 5; Gaps 1;

OY 1 MKLPVRLVLLFWIPVSGDVMTQSPVLPVTPGEPASISCRSSQSLAKSYGNTYLSW 60
DB 1 MEAPQQLFLLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSN-----LAW 55
OY 61 YLQKPGQSPQLLYIGISNRFSGVPDRFSGSGGTDFTLKISRVEADGVVYCCLOGTHQ 120
DB 56 YQKRGQSPRLIRDPASSRANGIPDRFSGSGGTDFTLKISRLEPEDPAVYCCQYSTSP 115
OY 121 PYFGGQTVETIKR 133
DB 116 PWTFGGQTVETIKR 128

Search completed: May 11, 1999, 12:20:09
Job time: 306 sec

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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:21:01 ; Search time 38.54 Seconds
(without 34 comments)

(without alignments)
197.544 Million cell updates/sec

Title: US-08-700-737-21

Sequence: 1 MKLPVRLVLLFWIPVSGG.....QPYTFGQGTKEIKRADAAP 138

Scoring table: BLOSUM62

Searched: 180763 seqs, 55169189 residues

Database :

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1: SPTRMBL_8.*
2:   sp_fungi.*
3:   sp_funaria.*
4:   sp_invertebrate.*
5:   sp_mammal.*
6:   sp_mhc.*
7:   sp_organelle.*
8:   sp_phase.*
9:   sp_plant.*
10:  sp_bacteria.*
11:  sp_podent.*
12:  sp_virus.*
13:  sp_vetbrate.*
14:  sp_unclassified.*
15:  sp_archaea.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	427	59.3	100	2	Q15535	Q15535 homo sapien
2	312	43.3	130	10	P80913	P80913 mus musculus
3	133	18.5	513	10	P97797	P97797 mus musculus
4	131.5	18.3	50	2	Q15533	Q15533 homo sapien
5	131	18.2	123	10	Q61243	Q61243 mus musculus
6	131	18.2	509	10	O08907	O08907 mus musculus
7	130	18.1	132	5	Q31175	Q31175 mus musculus
8	129	17.9	509	10	O35924	O35924 mus musculus
9	127.5	17.7	135	5	Q31174	Q31174 mus musculus
10	122	16.9	509	10	O88535	O88535 mus musculus
11	120	16.7	291	10	O88556	O88556 mus musculus
12	114.5	15.9	145	2	Q16237	Q16237 homo sapien
13	114.5	15.9	228	10	O70153	O70153 rattus norv
14	112.5	15.6	132	5	Q31177	Q31177 mus musculus
15	111.5	15.5	132	5	Q31176	Q31176 mus musculus
16	109	15.1	133	5	Q31178	Q31178 mus musculus
17	108.5	15.1	1031	2	Q15856	Q15856 homo sapien
18	108.5	15.1	1021	2	Q93033	Q93033 homo sapien
19	108	15.0	506	4	O46632	O46632 bos taurus
20	107.5	14.9	135	2	O99602	O99602 homo sapien
21	105.5	14.7	509	10	P97710	P97710 rattus norv
22	104.5	14.5	503	2	P78324	P78324 homo sapien
23	104	14.2	134	5	Q31180	Q31180 mus musculus
24	102.5	14.2	210	4	P79336	P79336 felis silve
25	102	14.2	506	4	O46631	O46631 bos taurus
26	101.5	14.1	418	10	O70426	O70426 rattus norv
27	101	14.0	137	5	Q31181	Q31181 mus musculus
28	100.5	13.8	222	12	O90568	O90568 ginglymstoc
29	99.5	13.8	358	2	O00241	O00241 homo sapien

30	99.5	13.8	700	2	075054	075054	homo sapien
31	99.9	13.8	198	2	Q13970	Q13970	homo sapien
32	95.5	13.3	133	12	Q90553	Q90553	ginglymost
33	94.5	13.3	254	12	Q90557	Q90557	ginglymost
34	94.5	13.1	119	2	Q99599	Q99599	homo sapien
35	94.5	13.1	121	2	Q99600	Q99600	homo sapien
36	94	13.1	122	2	Q99603	Q99603	homo sapien
37	94	13.1	157	12	Q90539	Q90539	ginglymost
38	93	12.6	122	2	Q99604	Q99604	homo sapien
39	91	12.6	145	12	Q90555	Q90555	ginglymost
40	90.5	12.6	288	2	Q00517	Q00517	homo sapien
41	90	12.5	120	5	Q31212	Q31212	mus musculu
42	90	12.5	117	10	Q61863	Q61863	mus muscul
43	90	12.5	143	12	Q90537	Q90537	ginglymost
44	89	12.4	1273	3	O44928	O44928	caenorhabdi
45	89	12.4	423	3	P91572	P91572	caenorhabdi

ALIGNMENTS

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RESULT 1
015535 PRELIMINARY; PRT: 100 AA.
ID Q15535
AC Q15535;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE V KAPPA (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA KATO S., TACHIBANA K., TAKAYAMA N., KATAOKA H., YOSHIDA M.C.,
RA TAKANO T.;
RL SUBMITTED (SEP-1990) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: D90161; G1262585; -.
DR PFAM: PF00047; 1g; 1.1
FT NON_TER 1
FT NON_TER 100
SQ SEQUENCE 100 AA; 10871 MW; 06A1440D CRC32;

Query Match 59.3%; Score 427; DB 2; Length 100;
Best Local Similarity 83.0%; Pred. No. 3.6e-32;
Matches 83; Conservative 6; Mismatches 11; Indels 0; Gaps 0

Oy 21 DVMQMSPLSLPTVTEGEPASISCRSSQSLAKSYGNTYLSWYLOKRGQSPQLLIYGISNRF 80
Db 1 DVMQMTPLSLVTEGPGASISCKSIQSLHSDGKTYLYLOKRGQSPQLLIYEVSSRF 60

Oy 81 SGVPRFSGSGSGDTFTLKISRVEAEDGCVYYCICLQGTTHP 120
Db 61 SGVPRFSGSGSGDTFTLKISRVEAEDGCVYYCICGIIHP 100

RESULT 2
P80913 PRELIMINARY; PRT: 130 AA.
ID P80913
AC P80913;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V REGION PRECURSOR.
OS MUS MUSCULUS (MOUSE).
OC EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
CC SCUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA JANON K.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X79906; E269393; ALT_TERM.

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KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 130 IG KAPPA CHAIN V REGION.
 SO SEQUENCE 130 AA; 14124 MW; 1DC6F7D9 CRC32;

Query Match 43.3%; Score 312; DB 10; Length 130;
 Best Local Similarity 50.0%; Pred. No. 1.4e-21;
 Matches 67; Conservative 18; Mismatches 43; Indels 6; Gaps 2;

QY 1 MKLVRLLVLLFWIP--SGGDVMTQSPSLPTPEPPASISCRSSQSLAKSYGNTYL 58
 DB 1 MDFOVIFSLISASVMSRGQIVLTQSPAIMSASLDERVTCTASSVSSS---YL 56
 QY 59 SWYLOKPGSPOLLITGYSNFRSGGVDPFRSGSGDTFLKISRVEADVGYYCLOGTH 118
 DB 57 HWYQOKPSSPKRWITYSNLSASGVAPRFSGSGSTISLTISSMEADDAITYCHQYHR 116
 QY 119 QPYTFGGQTKVEIK 132
 DB 117 PPHTEGGGTKEIK 130

RESULT 3
 P97797 PRELIMINARY; PRT; 513 AA.

AC P97797; P97796;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SHP SUBSTRATE-1 PRECURSOR (SHP-1) (SHP-1).
 GN PTPNS1.
 OS MUS MUSCULUS (MOUSE).
 OC EMBRYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCUROGNATHI; MORIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 97223399.
 RA YAMAO T., MATOZAKI T., AMANO K., MATSUDA Y., TAKAHASHI N., OCHI F.,
 RA FUJIOKA Y., KASUGA M.;
 RT "Mouse and human SHP-1: molecular cloning of cDNAs and chromosomal
 localization of genes."
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 231:61-67(1997).
 CC -1- FUNCTION: BINDS TO THE SH2 DOMAINS OF PROTEIN-TYROSINE
 PHOSPHATASE 2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY
 VARIOUS MITOGENS AND CELL ADHESION. MAY ACT AS A DOCKING PROTEIN
 AND INDUCE TRANSLOCATION OF SHP-2 FROM THE CYTOSOL TO THE PLASMA
 MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN, ISOFORMS 1 AND 2,
 ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE
 SEQUENCE SHOWN HERE IS THAT OF ISOFORM 1.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 7.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 TWO C1-LIKE AND ONE V-LIKE DOMAINS.
 DR EMBL; D87968; G1864015;
 DR EMBL; D87967; G1864013;
 DR MGD; MGI:108563; PTPNS1.
 DR PPM; PFO0047; 1g; 3.
 KW SIGNAL; TRANSMEMBRANE; ALTERNATIVE SPLICING; IMMUNOGLOBULIN FOLD;
 KW GLYCOPROTEIN; SH3-BINDING; PHOSPHORYLATION.
 FT SIGNAL 1 26
 FT CHAIN 27 513
 FT DOMAIN 27 373 SHP SUBSTRATE-1.
 FT TRANSSEM 374 394 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 395 513 POTENTIAL.
 FT DOMAIN 51 124 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 167 234 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 234 336 IG-LIKE C1-TYPE DOMAIN.
 FT DOMAIN 270 336 IG-LIKE C1-TYPE DOMAIN.
 FT DOMAIN 440 443 SH2-BINDING (POTENTIAL).
 FT DOMAIN 450 456 SH3-BINDING (POTENTIAL).
 FT DOMAIN 464 467 SH2-BINDING (POTENTIAL).

FT DOMAIN 481 484 SH2-BINDING (POTENTIAL).
 FT DOMAIN 505 508 SH2-BINDING (POTENTIAL).
 FT MOD_RES 440 440 POTENTIAL.
 FT MOD_RES 464 464 POTENTIAL.
 FT MOD_RES 481 481 POTENTIAL.
 FT MOD_RES 505 505 POTENTIAL.
 FT CARBOHYD 54 54 POTENTIAL.
 FT CARBOHYD 92 92 POTENTIAL.
 FT CARBOHYD 168 168 POTENTIAL.
 FT CARBOHYD 180 180 POTENTIAL.
 FT CARBOHYD 205 205 POTENTIAL.
 FT CARBOHYD 209 209 POTENTIAL.
 FT CARBOHYD 246 246 POTENTIAL.
 FT CARBOHYD 271 271 POTENTIAL.
 FT CARBOHYD 293 293 POTENTIAL.
 FT CARBOHYD 302 302 POTENTIAL.
 FT CARBOHYD 312 312 POTENTIAL.
 FT CARBOHYD 320 320 POTENTIAL.
 FT CARBOHYD 345 345 POTENTIAL.
 FT CARBOHYD 367 367 POTENTIAL.
 FT VARSPLIC 425 428 MISSING (IN ISOFORM 2).
 SO SEQUENCE 513 AA; 56425 MW; 0F29251A CRC32;

Query Match 18.5%; Score 133; DB 10; Length 513;
 Best Local Similarity 31.5%; Pred. No. 0.00011;
 Matches 46; Conservative 25; Mismatches 53; Indels 22; Gaps 8;

QY 7 LVLVLL---FWIVSGDVMTQSPSLPTPEPPASISCRSSQSLAKSYGNTYL 62
 DB 15 LLLCLLASCCCTGVTGKELKVTQPEKSVSAADSTVLNCTLTSLPVG---PIRWY- 70
 QY 63 QKPGSPOLLITGYSN----RFGVDPFRSGSGSGDTFLKISRVEADVGYYCLO 115
 DB 70 RGVGGS-RLLISTFGHEPRTVNSD--ATKRNMFSTRISNVTEDAGTYCAVAFQK 126
 QY 116 GTHQPYT---FGQTKVEIKRADAP 138
 DB 127 GPSEPDTEIQSGGTEYVLAKPSP 152

RESULT 4
 ID Q15533 PRELIMINARY; PRT; 50 AA.

AC Q15533;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE DNA REARRANGED BY A T(2;8) TRANSLOCATION LEADING TO BURKITT'S LYMPHOMA
 DE IN THE CELL LINE J1 (CLONE J1P).
 OS HOMO SAPIENS (HUMAN).
 OC EMBRYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CARPININI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA KLOBECK H.G.;
 RL SUBMITTED (AUG-1987) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE OF 36-50 FROM N.A.
 RX MEDLINE; 87259967.
 RA KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
 RT "A segment insertion and region-directed somatic hypermutation in a
 kappa gene of a t(2;8) chromosomal translocation."
 RL NUCLEIC ACIDS RES. 15:4877-4888(1987).
 DR EMBL; X05929; E12675;
 SO SEQUENCE 50 AA; 5486 MW; 65586C19 CRC32;

Query Match 18.3%; Score 131.5; DB 2; Length 50;
 Best Local Similarity 48.1%; Pred. No. 1.3e-05;
 Matches 25; Conservative 12; Mismatches 10; Indels 5; Gaps 1;

QY 21 DVMTQSPSLPTPEPPASISCRSSQSLAKSYGNTYLSWYLOKPGSPOLL 72


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DB 4 DIOMTQSPSSLSASVGDVATVISCQASQDI-----SNVLMWYQKPKAKRL 50
RESULT 5
ID 061243 PRELIMINARY: PRT: 123 AA.
AC 061243;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-B LYMPHOCYTE PROTEIN 3 (8HS20 PROTEIN).
GN VPREB3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RC MEDLINE: 93259124.
RX SHIRASAMA T., OHNISHI K., HAGIWARA S., SHIGEMOTO K., TAKEBE Y.,
RA RAJWASY K., TAKEMORI T.;
RT "A novel gene product associated with mu chains in immature B cells.";
RL EMBL J 121827-1834(1993).
DR EMBL: D13208; G286065; -.
DR MGD: MGI:98938; VPREB3.
DR PFAM: PF00047; 1g; 1.
FT CHAIN 20
FT SEQUENCE 123 AA; 13400 MW; DA2A70D3 CRC32;

Query Match 18.2%; Score 131; DB 10; Length 123;
Best Local Similarity 35.3%; Pred. No. 3.8e-05;
Matches 42; Conservative 18; Mismatches 51; Indels 8; Gaps 5;

QY 8 LVLLFWIVSGDVMTQSPVLSPTPEPASPISCRSSQSLAKSYGNTLYSLWLPQ 67
DB 7 LPLLIGTFVAVFQPTLT-PPAFSVFPGQDAHLSCITNSQAHATA-GDIGVSYQOQPS 64
QY 68 SPOLLITVIGISN--RFSGVPDRFSG--SGSGDTFLKISRVEADVGYVC-LQGHOP 120
DB 65 AHHLYTYAEHEHYRPADIPDRFSATVDAAHNACILITISVLPEDDADYFCSTIAITFP 123

RESULT 6
ID 008907 PRELIMINARY: PRT: 509 AA.
AC 008907;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE BRAIN IMMUNOLOGICAL-LIKE WITH TYROSINE-BASED MOTIFS
DE (BIT, COMPLETE CDS).
GN BIT.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RC MEDLINE: 97230468.
RX OHNISHI H., KUBOTA M., SANO S.;
RT "BIT (Bit) maps to mouse chromosome 2.";
RL GENOMICS 40:504-506(1997).
DR EMBL: D85785; D1021208; -.
DR MGD: MGI:107947; BIT.
DR PFAM: PF00047; 1g; 3.
FT SEQUENCE 509 AA; 56033 MW; 4C020C08 CRC32;

Query Match 18.2%; Score 131; DB 10; Length 509;
Best Local Similarity 31.5%; Pred. No. 0.00017;
Matches 46; Conservative 24; Mismatches 54; Indels 22; Gaps 8;

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QY 7 LVLL----FWIVSGDVMTQSPVLSPTPEPASPISCRSSQSLAKSYGNTLYSLWLP 62
DB 15 LLLCLLSASCFCGTGATGTEVKYTOPEKSYVAAGSTILNCTVSLPVG-----PIRWT- 70
QY 63 QKPGSPOLLITVIGISN--RFSGVPDRFSGSGSDTFLKISRVEADVGYVC-L--QGH 115
DB 70 RGVGOS-RLLIYSFTGEHPRVRNYS--TTRKNMDFSRISNVTPEAGTYVCVKFOR 126
QY 116 GTHOPYT--FGSGTKVEIKRADAP 138
DB 127 GSSEPDTEIQSGGTEVYVLAKPSPP 152

RESULT 7
ID 031175 PRELIMINARY: PRT: 132 AA.
AC 031175;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MHC CLASS II I-A-ALPHA MRNA (H-2b), 5' END, HYBRIDOMA BBL.D5 PRECURSOR
DE (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 87224052.
RX SPINELLA D.G., HANSEN T.H., WALSH W.D., BEHIKE M.A., TILLINGHAST J.P.,
RA CHOU H.S., WHITELEY P.J., KAPP J.A., PIERCE C.W., SHEVACH E.M.,
RA LOH D.Y.;
RT "Receptor diversity of insulin-specific T cell lines from C57BL (H-2b)
RT mice.";
RL J. IMMUNOL. 138:3991-3995(1987).
DR EMBL: M16576; G19456; -.
DR PFAM: PF00047; 1g; 1.
FT SIGNAL; MHC.
FT NON_TER 1
FT SIGNAL 1
FT SIGNAL <1 19 POTENTIAL.
FT CHAIN 20 >132 POTENTIAL.
FT NON_TER 132
FT SEQUENCE 132 AA; 14319 MW; 32E47F9C CRC32;

Query Match 18.1%; Score 130; DB 5; Length 132;
Best Local Similarity 31.6%; Pred. No. 5e-05;
Matches 42; Conservative 21; Mismatches 58; Indels 12; Gaps 5;

QY 4 PYRLVLLFWIVSGDVMTQSPVLSPTPEPASPISCRSSQSLAKSYGNTLYSLWLPQ 63
DB 4 PGFVAIILLILRTIGDSVTQTGQVT--VSESKLILNCTYS--AVSIGPNLFWYR 58
QY 64 KPQSPOLLITVIGISNRFSGVPDRFSG--SGSGDTFLKISRVEADVGYVC-L--QGH 118
DB 59 YIGEPOLLILAKYITAGQSGSSRGFEATYKKAETSHLAKASVQESDSAVTYCALNSGT 118
QY 119 QPTFGQGTKEVI 131
DB 119 Q--RFGTKILOV 129

RESULT 8
ID 035924 PRELIMINARY: PRT: 509 AA.
AC 035924;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR
DE (P84).
GN PTPNS1.
OS MUS MUSCULUS (MOUSE).

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98012243.
 RA COMO S., WENG W., OLINSKY S., ISHWAD P., MI Z., HEMPEL J., WATINS S.,
 RA LAGENAU C.F., NARAYANAN V.,
 RT "The murine p84 neural adhesion molecule is SHPS-1, a member of the
 RT phosphatase-binding protein family.";
 RT J. NEUROSCI. 17:8702-8710(1997).
 DR EMBL: U89694; G2580535; -
 DR MGD: MGI:108563; PTPNS1.
 DR PFAM: PF00047; 19; 3.
 KW SIGNAL.
 FT CHAIN 1 31 POTENTIAL.
 FT CHAIN 32 509 P84.
 SQ SEQUENCE 509 AA; 56056 MW; 3A781050 CRC32;

Query Match 17.9%; Score 129; DB 10; Length 509;
 Best Local Similarity 30.8%; Pred. No. 0.00026;
 Matches 45; Conservative 25; Mismatches 54; Indels 22; Gaps 8;

QY 7 LVLALL----FWIPVSGDVMTQSPSLPTPGEPASISCRSSQSLAKSYGNTLYSYL 62
 DB 15 LCLLLASCFCTGATGKELKVTQPEKSVSAAGDSTVNCILITSLPVG----PIKRY- 70
 QY 63 QKPGQSPQLLIYGISN----RFGVDPDRFSGSGSTDFTLKISRVEADGVYCYCL---Q 115
 DB 70 KGVGGS-RLILYSGFGEHPRVRNVSD--TKRNMNDSIRISNVTPEAGIYCYVKFOR 126
 QY 116 GTHOPYT---FGQGTKEIKRADAP 138
 DB 127 GSSEPDTEIQSGGTEYVLAKEPSP 152

RESULT 9
 Q31174 PRELIMINARY; PRT; 135 AA.
 AC Q31174;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MHC CLASS II I-A-ALPHA MRNA
 DE (H-2B), 5' END, HYBRIDOMA DA.33.C2 PRECURSOR (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87224052.
 RA SPINELLA D.G., HANSEN T.H., WALSH W.D., BEHLKE M.A., TILLINGHAUT J.P.,
 RA CHOI H.S., WHITELEY P.J., KAPP J.A., PIERCE C.W., SHEVACH E.M.,
 RA LOH D.Y.,
 RT "Receptor diversity of insulin-specific T cell lines from C57BL (H-2b)
 RT mice.";
 RT J. IMMUNOL. 138:3991-3995(1987).
 DR EMBL: M16675; G199454; -
 DR PFAM: PF00047; 19; 1.
 KW SIGNAL; MHC.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 >135 POTENTIAL.
 FT NON_TER 135 135
 SQ SEQUENCE 135 AA; 14646 MW; F60E6A2 CRC32;

Query Match 17.7%; Score 127.5; DB 5; Length 135;
 Best Local Similarity 29.0%; Pred. No. 8.6e-05;
 Matches 40; Conservative 23; Mismatches 52; Indels 23; Gaps 5;

QY 7 LVLALLFWIPVSGDVMTQSPSLPTPGEPASISCRSSQSLAKSYGNTLYSYLQKPG 66
 DB 2 LVTVMFLIGRTHGDSVI-OMOGVTFSENDSLFINCTYSTT-----GYPLIFWYVOISG 60

QY 67 QSPOLLIV-----GISNFGSGVDPFRSGSGTDFTLKISRVEADGVYCYCL----- 115
 DB 61 EGROLLQVTTANKKSSRFEATYDK-----GTSFHLQKTSVQIDSAVYICATSDLS 115
 QY 115 QGTHOPYTGGGTKEIK 132
 DB 116 GGSNAKLAFGKGTLSVK 133

RESULT 10
 Q31174 PRELIMINARY; PRT; 509 AA.
 AC Q31174;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE INHIBITORY RECEPTOR SHPS-1 LONG ISOFORM.
 GN SHPS1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-THYMUS;
 RA VEILLETTE A., THIBAUDEAU E., LATOUR S.,
 RT "High expression of inhibitory receptor SHPS-1 and its association
 RT with protein tyrosine phosphatase SHP-1 in macrophages.";
 RT J. BIOL. CHEM. 0:0-0(1998).
 DR EMBL: AF072543; G3273916; -
 SQ SEQUENCE 509 AA; 55986 MW; 34F9E651 CRC32;

Query Match 16.9%; Score 122; DB 10; Length 509;
 Best Local Similarity 29.3%; Pred. No. 0.0011;
 Matches 43; Conservative 25; Mismatches 55; Indels 24; Gaps 8;

QY 7 LVLALL----FWIPVSGDVMTQSPSLPTPGEPASISCRSSQSLAKSYGNTLYSYL 62
 DB 15 LCLLLASCFCTGATGKELKVTQPEKSVSAAGDSTVNCILITSLPVG----PIKRY- 70
 QY 63 QKPGQSPQLLIYGISN----RFGVDPDRFSGSGSTDFTLKISRVEADGVYCYCL--- 115
 DB 70 --KGVGSPRLILYSGFGEHPRVRNVSD--TKRNMNDSIRISNVTPEAGIYCYVKQ 125
 QY 115 QGTHOPYT---FGQGTKEIKRADAP 138
 DB 126 KGSSEPDTEIQSGGTEYVLAKEPSP 152

RESULT 11
 Q31174 PRELIMINARY; PRT; 291 AA.
 AC Q31174;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE INHIBITORY RECEPTOR SHPS-1 SHORT ISOFORM.
 GN SHPS1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-THYMUS;
 RA VEILLETTE A., THIBAUDEAU E., LATOUR S.,
 RT "High expression of inhibitory receptor SHPS-1 and its association
 RT with protein tyrosine phosphatase SHP-1 in macrophages.";
 RT J. BIOL. CHEM. 0:0-0(1998).
 DR EMBL: AF072544; G3273918; -
 SQ SEQUENCE 291 AA; 31735 MW; C892D685 CRC32;

Query Match 16.7%; Score 120; DB 10; Length 291;
 Best Local Similarity 30.0%; Pred. No. 0.00094;
 Matches 42; Conservative 24; Mismatches 50; Indels 24; Gaps 8;

QY 7 LVLLVLT-----FWIPVSGDVMTQSPSLPTVPGEPAISCSRSSQSLAKSYGNTYLSWYL 62
 DB 15 LVLLVLTASCFCTGATCKELKATVOPKSVSAADSTVLTCTLSLTPVG---PIRWY- 70
 QY 63 QKPGQSP-QLLIYGISN-----RFGVDPDRFSGSGSDTFLTKISRVEADVGYYCYCL- 115
 DB 70 --RGVGSRLIITSFAEYYPRIKNSVD--TKRNNMDFSRISNVPADAGIYCYKFKQ 125
 QY 115 QGTHQPYT---FSGGTKEI 131
 DB 126 KGSSEPTETIOSGGTEYV 145

RESULT 12
 ID 016237 PRELIMINARY; PRT; 145 AA.
 AC 016237;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE VPRE-B PROTEIN.
 GN VPRE-B.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 95021318.
 RA GUELA-FONLUP V., BOSSY D., ALZARI P., FUMOUX F., FOUGEREAU M.,
 RA SCHIEF C.;
 RT "The human pre-B cell receptor: structural constraints for a tentative
 RT model of the pseudo-light (psi L) chain.";
 RL EMBL; S74019; 6693811; -
 DR PRAM; PF00047; 19; 1.
 SQ SEQUENCE 145 AA; 16605 MW; 7E7002CB CRC32;

Query Match 15.9%; Score 114.5; DB 2; Length 145;
 Best Local Similarity 30.0%; Pred. No. 0.0014;
 Matches 36; Conservative 21; Mismatches 44; Indels 19; Gaps 7;

QY 9 VLLFWIPVSG-GDVMTQSPSLPTVPGEPAISCS--RSSQSLAKSYGNTYLSWYLQKP 65
 DB 6 VLLFWIPVCTGCGPQPLHQPAMSSALGTTIRLTCTLRNDHDI---GYSVYMYOQRP 61
 QY 66 GSPOLLIT--YGISNRFSG--VPPDRFSGSGSGTDF-----LKISRVEADVGYYCYCLOG 116
 DB 62 GHPREFLRFSQSDKSGQFOVPPRFSGS---KDYARNRGLTSLSELOPEDENYTCAMG 118

RESULT 13
 ID 070153 PRELIMINARY; PRT; 228 AA.
 AC 070153;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE B29/TG-BETA/CD79B.
 GN B29/TG-BETA.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIDUOGNATHI; MORIDAE; MORINAE; RATTUS.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RX MEDLINE; 98207252.
 RA NAKAZATO S., NOMOTO K., KAZAHARI K., ONO M.;
 RT "Physical linkage of the B29/Ig-beta (CD79b) gene to the skeletal

RT muscle, sodium-channel, and growth hormone genes in rat and human.";
 RL GENOMICS 48:363-368(1998).
 DR EMBL; AB004831; D1026583; -
 SQ SEQUENCE 228 AA; 25865 MW; 03F8D7C6 CRC32;

Query Match 15.9%; Score 114.5; DB 10; Length 228;
 Best Local Similarity 28.3%; Pred. No. 0.0023;
 Matches 39; Conservative 23; Mismatches 45; Indels 31; Gaps 7;

QY 8 LVLLFWIPVSGDVMTQSPSLPTVPGEPAISCSRSSQSLAKSYGNTYLSWYL 57
 DB 17 LVLLVLTGSEVPV---AWTKSD-QPPIFGSPCSKIQWHPFAAKRSSWYKFCHTDYSG 71
 QY 57 YLSWYLQKPGQSPOLLITYGISNRFSGVDP--RFGSGSGSDTFLTKISRVEADVGYYCYCL 114
 DB 72 VMTWFRKGNQROLEF-----PEDGHISQFRNLSVYTLTQNIQYEDNGITFCQ 121
 QY 115 Q---GTHQPYTFSGGTKV 129
 DB 122 QKCNSTEPDVTDCGTSL 139

RESULT 14
 ID 031177 PRELIMINARY; PRT; 132 AA.
 AC 031177;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MHC CLASS II I-A-ALPHA RNA
 DE (H-2B), 5' END, HYBRIDOMA AF.3.G7 PRECURSOR (FRAGMENT).
 OS MUS MUSCULUS (MUSE).
 OC EUKARYOTA; METAZOA; CHORATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIDUOGNATHI; MORIDAE; MORINAE; MUS.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 87224052.
 RA SPINELLA D.G., HANSEN T.H., WALSH W.D., BEHKE M.A., TILLINGHAST J.P.,
 RA CHOU H.S., WHITELEY P.J., KARP J.A., PIERCE C.W., SHEVACH E.M.,
 RA LOH D.Y.;
 RT "Receptor diversity of insulin-specific T cell lines from C57BL (H-2b)
 RT mice.";
 RL J. IMMUNOL. 138:3991-3995(1987).
 DR EMBL; M16578; G199460; -
 DR PRAM; PF00047; 19; 1.
 KW SIGNAL; MHC.
 FT SIGNAL. 1 19
 FT CHAIN 20 >132 POTENTIAL.
 FT NON_TER 132 132
 SQ SEQUENCE 132 AA; 14674 MW; 9364DDAD CRC32;

Query Match 15.6%; Score 112.5; DB 5; Length 132;
 Best Local Similarity 30.7%; Pred. No. 0.002;
 Matches 42; Conservative 16; Mismatches 58; Indels 21; Gaps 6;

QY 7 LVLLVLT-----FWIPVSGDVMTQSPSLPTVPGEPAISCSRSSQSLAKSYGNTYLSWYL 61
 DB 2 LVVLTSLFLGIFFLDVTQTV--SQSDAHYVEGSGVELEKCYSYG-----GSITLSWY 54
 QY 62 LQKPGQSPOLLITYGISNR-----FSGVDPDRFSGSGSDTFLTKISRVEADVGYYCYCLOG 116
 DB 55 IOHHGHLQFLKYYSGNPVYGVNGEAELEFSSDS--STHLKASVHMSDAVYFCAYR 112
 QY 117 THQ--PYTFSGGTKVEI 131
 DB 113 TASLGKLFQGTQVYV 129

RESULT 15
 ID 031176 PRELIMINARY; PRT; 118 AA.
 ID 031176

OM protein - protein search, using sw model

Title: US-08-700-737-21

Sequence: 1 MKLPVRLVLLFWIPVSGG.....QPYTFGGGTKEIKRADAAP 138

Scoring table: BLOSUM62

Searched: 162890 seqs, 20225328 residues

Database : A_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	712	98.9	138	1	W53812	Light chain of a h
2	646	89.7	140	1	W53817	Consensus protein
3	616	85.6	132	1	W53814	Murine Act-1 light
4	582.5	80.9	131	1	R52822	Humanised murine K
5	582.5	80.9	131	1	R70470	Humanised anti-KC-
6	582.5	80.9	149	1	W03199	Anti-idiotypic mono
7	579	80.4	239	1	W71876	Anti-human Fas hum
8	579	80.4	239	1	W71878	Anti-human Fas hum
9	575	79.9	239	1	W71877	Anti-human Fas hum
10	575	79.9	238	1	W71879	Anti-human Fas hum
11	574.5	79.8	238	1	W14962	3F4 Human IgG4 exp
12	574.5	79.8	238	1	W14937	Murine anti-porcine
13	570.5	79.2	131	1	W34518	Variable kappa cha
14	570.5	79.2	238	1	W31752	L chain subunit of
15	570.5	79.2	238	1	W71889	Anti-human Fas mon
16	564.5	78.4	131	1	R52806	Humanised murine B
17	562.5	78.1	172	1	R15199	R6-5-D6 anti-ICAM-
18	561.5	78.0	140	1	W68492	Variable light cha
19	558	77.5	150	1	R11598	Murine monoclonal
20	549.5	76.3	131	1	R32241	Chimeric MAb light
21	549.5	76.3	131	1	R31567	BR55-2 light chain
22	545.5	75.8	131	1	R52772	Murine KC-4 immuno
23	545.5	75.8	131	1	R52790	Murine KC-4 immuno
24	545.5	75.8	131	1	R70457	Variable region of
25	545.5	75.8	132	1	R60867	Variable region of
26	543.5	75.5	131	1	R32245	BR55-2 murine IgG3
27	538.5	74.8	173	1	R15059	Murine anti-ICAM m
28	536	74.4	135	1	R54054	Sequence of the VL
29	536	74.4	135	1	W01525	Monoclonal antibody
30	536	74.4	135	1	W24989	Monoclonal antibody
31	535	74.3	239	1	W01819	Primalised anti-hu
32	535	74.3	239	1	W63762	Macaque primatized
33	535	74.3	129	1	W71887	Anti-Fas MAb Ch11
34	532.5	74.0	238	1	R93554	Monoclonal antibody
35	530	73.6	116	1	W76126	Human ICR-1 V-K
36	530	73.6	116	1	W71256	Humanised murine a
37	528.5	73.4	131	1	R09444	Co-1 Light Chain v
38	528.5	73.4	131	1	W06214	Mab Co-1 light cha
39	522	72.5	112	1	R32239	Humanised MAb ligh
40	522	72.5	112	1	W27145	Humanised MAb ligh
41	522	72.5	112	1	W54015	Mature light chain
42	517.5	71.9	131	1	R52788	Human Anti-CD4 ant
43	517.5	71.9	131	1	R52770	Murine B7E-3 immu

ALIGNMENTS

Query Match	Best Local Similarity	Score	DB 1:	Length	DB 2:
Match 137: Conservative	99.38%	Pred. NO. 1.1e-45;	1;	Indels 0;	Gaps 0;
1 MKLPRLLVLLFLFVPGSGDVVMQSPSLPVTGEPASICRSSQSILAKSYGNTYLSM	60				
1 MKLPRLLVLLFLFVPGSGDVVMQSPSLPVTGEPASICRSSQSILAKSYGNTYLSM	60				
61 YLQKFGSGPQLLIYGISNRFSGVPPDRFSGSGSGDFTLKISFVEADGVYVYCCLOGTHQ	120				
61 YLQKFGSGPQLLIYGISNRFSGVPPDRFSGSGSGDFTLKISFVEADGVYVYCCLOGTHQ	120				
121 YTFGGGTKEVKRRADAP	138				
121 YTFGGGTKEVKRRADAP	138				
121 YTFGGGTKEVKRRADAP	138				

RESULT 1

W53812 standard; Protein; 138 AA.

W53812; (first entry)

14-JUL-1998 Light chain of a humanised murine Act-1 antibody.

Mouse: Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MacCAM-1; humanised antibody; murine antigen binding region; Inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.

Synthetic.

Mus sp.

Homo sapiens.

Key

Peptide

Protein

Location/Qualifiers

1..20

/note="signal peptide"

21..138

/note="mature protein"

W09806248-A2.

19-FEB-1998.

06-AUG-1997; U13884.

15-AUG-1996; US-700737.

(LEUK-1) LEUKOSITE INC.

Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ, Saldanna J; WPI; 98-159172/14.

N-PSDB; V20075.

Humanised immunoglobulin reactive with alpha-4-beta-7 integrin - used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis

Claim 15; Fig 12; 145pp; English.

The present sequence represents the light chain of humanised murine antibody Act-1. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MacCAM-1) is a ligand of this particular integrin. The Act-1 antibody interferes with alpha4-beta7 integrin binding to MacCAM-1, which is present of high endothelial venules in muscosal lymph nodes. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.

Sequence 138 AA;

RESULT 2

W53817 standard; Protein; 140 AA.

AC W53817;
 DT 14-JUL-1998 (first entry)
 DE Consensus protein sequence of the murine variable light chain region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KM Muscosa adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KM leukocyte infiltration of tissue; treatment; inflammatory disease;
 OS Mus sp.
 FH Key
 FT Peptide
 FT Protein
 FT /note- "signal peptide"
 FT /note- "mature protein"
 PN W0906248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI: 98-159172/14.
 DR N-PSDB: V20086.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1: Fig 3: 145pp; English.
 CC The present sequence represents the consensus amino acid sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse light chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosa adressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in muscosa
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20083-84. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 140 AA;

Query Match 89.7%; Score 646; DB 1; Length 140;
 Best local similarity 88.4%; Pred. No. 7.5e-41;
 Matches 122; Conservativity 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGGVNTQSPSLPTPGEPAISCRSSSGLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGGVNTQSPSLPTPGEPAISCRSSSGLAKSYGNTYLSW 60
 QY 61 YLQKPGSPOLLITIGISNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYICLQGTROP 120
 DB 61 YLHKGSPOLLITIGISNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYICLQGTROP 120
 QY 121 YTFGGGTVEIKRADAP 138
 DB 121 YTFGGGTVEIKRADAP 138

RESULT 3
 ID W53814 standard; Protein; 132 AA.
 AC W53814;
 DT 14-JUL-1998 (first entry)
 DE Murine Act-1 light chain variable region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KM Muscosa adressin cell adhesion molecule-1; MadCAM-1;

KW humanised antibody; murine antigen binding region; inhibition;
 KM leukocyte infiltration of tissue; treatment; inflammatory disease;
 OS Mus sp.
 FH Key
 FT Peptide
 FT Protein
 FT /note- "signal peptide"
 FT /note- "mature protein"
 PN W0906248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI: 98-159172/14.
 DR N-PSDB: V20077.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Claim 23: Fig 7: 145pp; English.
 CC The present sequence represents the light chain variable region of
 CC murine antibody Act-1. Act-1 is active against human alpha4-beta7
 CC integrin. Muscosa adressin cell adhesion molecule-1 (MadCAM-1) is a
 CC ligand of this particular integrin. The Act-1 antibody interferes with
 CC alpha4-beta7 integrin binding to MadCAM-1, which is present of high
 CC endothelial venules in muscosa lymph nodes. Humanised Act-1 can be used
 CC to inhibit the interaction of cells bearing alpha4-beta7 with cells
 CC bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 SQ Sequence 132 AA;

Query Match 85.6%; Score 616; DB 1; Length 132;
 Best local similarity 87.9%; Pred. No. 1.1e-38;
 Matches 116; Conservativity 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGGVNTQSPSLPTPGEPAISCRSSSGLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGGVNTQSPSLPTPGEPAISCRSSSGLAKSYGNTYLSW 60
 QY 61 YLQKPGSPOLLITIGISNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYICLQGTROP 120
 DB 61 YLHKGSPOLLITIGISNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYICLQGTROP 120
 QY 121 YTFGGGTVEIKRADAP 132
 DB 121 YTFGGGTVEIKRADAP 132

RESULT 4
 ID R52822 standard; Protein; 131 AA.
 AC R52822;
 DT 25-JAN-1995 (first entry)
 DE Humanised murine KC-4 immunoglobulin light chain V-region.
 KW Immunoglobulin variable domain; primer; polymerase chain reaction;
 KM chimeric antibody; human mammary fat globule; human breast carcinoma;
 KW murine anti-HMFG monoclonal antibody KC-4; humanised analogue.
 OS Chimeric Mus musculus.
 PN W09411509-A.
 PD 26-MAY-1994.
 PF 16-NOV-1993; U11445.
 PR 16-NOV-1992; US-977696.
 PR 30-SEP-1993; US-129930.
 PR 08-OCT-1993; US-134346.
 PA (CANC-) CANCER RES FUND CONTRA COSTA.
 PI Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;
 DR WPI: 94-183510/22.

DR N-PSDB: 062803.
 PT New analogue peptide(s) comprising antibody variable regions -
 PT used to develop prods. for use in the detection, diagnosis,
 PT therapy and prevention of neoplasms
 PS Example 75: Page 95: 109pp: English.
 CC This sequence represents a humanised murine anti-human carcinoma
 CC KC-4 antibody light chain variable region. The humanised antibody is
 CC useful for carcinoma therapy and diagnosis and for in vivo imaging
 CC of neoplastic cells. It is also of use in inhibiting the growth of
 CC a primary or metastasised neoplasm.
 SQ Sequence 131 AA;

Query Match 80.9%; Score 582.5; DB 1; Length 131;
 Best Local Similarity 84.1%; Pred. No. 3e-36;
 Matches 11; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKLPLVRLVLLFMFIPVSGGVMTQSLPVPPEPASISCRSSGSIANSYGTYSW 60
 DB 1 MKLPLVRLV-LMFVIRPSSSDVMTQPLSLPVPPEPASISCRSSGSIANSYGTYSW 59
 QY 61 YLQKPGSPOLLIKYKVSIRFSGVDPDRFSGSGGTDFTLKISRVEADYGVYTCLOGTHOP 120
 DB 60 YLQKPGSPOLLIKYKVSIRFSGVDPDRFSGSGGTDFTLKISRVEADYGVYTCLOGTHOP 119
 QY 121 YTFGGGTLEIK 132
 DB 120 YTFGGGTLEIK 131

RESULT 5
 R70470
 ID R70470 standard; Protein; 131 AA.
 AC R70470;
 DT 27-OCT-1995 (first entry)
 DE Humanised anti-KC-4 antibody VL FR-HZ.
 KW Anti-KC-4 antibody; humanised antibody; cancer.
 OS Synthetic.
 PN WO9510776-A.
 PD 20-APR-1995.
 PF 16-NOV-1993; U11444.
 PR 08-OCT-1993; US-134346.
 PA (CANC.) CANCER RESEARCH FUND CONTRA COSTA.
 PI Certani RL, Docunto JFR, Peterson JA;
 DR N-PSDB: 087533.
 PT New humanised anti-KC-4 monoclonal antibody - used for detection of
 PT cancer cells. In vivo imaging, ex-vivo purging and treatment of
 PT cancers
 PS Claim 2: Table 24, Page 51: 61pp: English.
 CC Hybridomas were prepd. based on the anti-KC-4 mouse hybridoma ATCC
 CC HB 8710 (US4708930). The murine variable regions were modified at
 CC particular AAs by PCR to provide humanised sequences. The anti-KC-4
 CC humanised DNA sequences for the VH and VL segments are shown in
 CC Q87534 and Q87533 respectively. Plasmid constructions comprising
 CC the humanised variable regions and the human constant regions were
 CC then used to transfect SP2/0-Ag14 myeloma cells to produce the
 CC humanised anti-KC-4 mAbs. The deduced AA sequences of the
 CC humanised anti-KC-4 variable light and heavy chains are given in
 CC R70470 and R70471 respectively.
 SQ Sequence 131 AA;

Query Match 80.9%; Score 582.5; DB 1; Length 131;
 Best Local Similarity 84.1%; Pred. No. 3e-36;
 Matches 11; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKLPLVRLVLLFMFIPVSGGVMTQSLPVPPEPASISCRSSGSIANSYGTYSW 60
 DB 1 MKLPLVRLV-LMFVIRPSSSDVMTQPLSLPVPPEPASISCRSSGSIANSYGTYSW 59
 QY 61 YLQKPGSPOLLIKYKVSIRFSGVDPDRFSGSGGTDFTLKISRVEADYGVYTCLOGTHOP 120
 DB 60 YLQKPGSPOLLIKYKVSIRFSGVDPDRFSGSGGTDFTLKISRVEADYGVYTCLOGTHOP 119

DB 60 YLQKPGSPOLLIKYKVSIRFSGVDPDRFSGSGGTDFTLKISRVEADYGVYTCLOGTHOP 119
 QY 121 YTFGGGTLEIK 132
 DB 120 YTFGGGTLEIK 131

RESULT 6
 W03199
 ID W03199 standard; Protein; 149 AA.
 AC W03199;
 DT 26-FEB-1997 (first entry)
 DE Anti-Idiotypic monoclonal antibody 1A7 variable light chain.
 KW Murine; mouse; anti-Idiotypic; monoclonal antibody; Mab; 1A7;
 KW variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
 KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
 KW malignant melanoma; soft tissue sarcoma; small cell carcinoma;
 KW vaccine; treatment; palliate; detection; diagnosis;
 KW recombinant production; purification; probe; primer; assay;
 OS Mus musculus.
 FH Key location/Qualifiers
 FT peptide 1..19
 FT /label= sig_peptide
 FT region 20..42
 FT /note="framework region 1"
 FT region 43..58
 FT /note="complementarity determining region 1"
 FT region 59..73
 FT /note="framework region 2"
 FT region 74..80
 FT /note="complementarity determining region 2"
 FT region 81..112
 FT /note="framework region 3"
 FT region 113..121
 FT /note="complementarity determining region 3"
 FT region 122..131
 FT /note="framework region 4"
 PN WO9622373-A2.
 PD 25-JUL-1996.
 PR 17-JAN-1996; U00882.
 PR 17-JAN-1995; US-372676.
 PR 16-JAN-1996; US-372676.
 PA (KENT) UNIV KENTUCKY.
 PI Chatterjee M, Chatterjee SK, Foon KA;
 DR N-PSDB: T31332.
 PT Monoclonal antibody 1A7 and related polynucleotide(s) and
 PT polypeptide(s) - useful to treat or palliate a GD2-associated
 PT disease, e.g. melanoma and glioma
 PS Claim 8: Fig 1: 141pp: English.
 CC The present sequence is that of the murine anti-Idiotypic monoclonal
 CC antibody (Mab) 1A7 variable light chain. Mab 1A7 was raised against
 CC the anti-ganglioside 2 (GD2) Mab 14G2a, which binds an unique
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
 CC of the lung, Mab 1A7, or its cDNA can be used in a vaccine to treat
 CC or palliate such diseases. They can also be used to reduce the
 CC risk of recurrence of a clinically detectable tumour, and detect an
 CC anti-GD2 Ab bound to a tumour cell.
 CC Mab 1A7 overcomes immune tolerance and induces an immune response
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and
 CC GD2-specific cells (cellular response). It can be used to purify
 CC anti-1A7 (Ab3), anti-GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or
 CC anti-GD2 in a sample or measure the level of cellular anti-1A7 or
 CC anti-GD2 activity.
 CC The cDNA can be used in expression systems for 1A7 prod., and in
 CC the prep. of probes and primers to respectively assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.
 SQ Sequence 149 AA;

sequences including the humanized antibodies are claimed, as are vectors such as pKappaPXY2-58. Including the VI-K1 nucleotide sequence (see V61359), and host cells such as *Escherichia coli*.

CC expressing Fas (e.g. synoviocytes) and are useful in the treatment

CC CH11. The humanised sequence was designed following selection of
 CC donor residues from CH11 to be grafted onto acceptor molecule
 CC PM6410/C1. 4 light chain sequences (see W1876-79) have been
 CC designed, and each can be used in combination with either of 2
 CC heavy chain sequences (see W1880-81) to provide novel, claimed
 CC humanised CH11 IgM antibodies that lack a J chain. These humanised
 CC anti-human Fas antibodies are capable of inducing apoptosis in cells
 CC expressing Fas (e.g. synovialocytes) and are useful in the treatment
 CC of autoimmune disease and chronic rheumatoid arthritis. DNA
 CC sequences encoding the humanised antibodies are claimed, as are
 CC vectors such as pKparrF2-52 including the VL-RF nucleotide
 CC sequence (see V61362), and host cells such as Escherichia coli
 CC pKparrF2-52 (FERM BP-5862).
 SQ Sequence 239 AA;

Query Match 79.8%; Score 575; DB 1; Length 239;
 Best Local Similarity 80.4%; Pred. No. 1.9e-35;
 Matches 11; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEPASISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEPASISCRSSQSLAKSYGNTYLSW 60
 OY 61 YLQKPGQSPOLLITGYSNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 DB 61 YLQKPGQSPOLLITGYSNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 OY 61 YLQKPGQSPOLLITGYSNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 DB 61 YLQKPGQSPOLLITGYSNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 OY 121 YTFGGGTKEIKRADAAP 138
 DB 121 YTFGGGTKEIKRADAAP 138
 OY 121 YTFGGGTKEIKRADAAP 138
 DB 121 YTFGGGTKEIKRADAAP 138

RESULT 11

W14942
 ID W14942 standard; Protein: 238 AA.

AC W14942:
 DT 16-JUN-1997 (first entry)
 DE 3F4 Human IgG4 expression plasmid insert product (light chain).
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KM Vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KM chimeric antibody; diagnosis.
 OS Mus sp.
 PN MO9711971-A1.
 PD 03-APR-1997.
 PF 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matlis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR N-PSDB: T62938.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure: Page 65-66; 105pp; English.
 CC Heavy chain (W14941) and light chain (W14942) sequences
 CC correspond to murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 3F4 (see also W1937-38). They
 CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
 CC also T62938). A chimeric antibody specific for porcine VCAM can be
 CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 SQ Sequence 238 AA;

Query Match 79.8%; Score 574.5; DB 1; Length 238;
 Best Local Similarity 81.2%; Pred. No. 2.1e-35;
 Matches 11; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

OY 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEPASISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEPASISCRSSQSLAKSYGNTYLSW 59
 OY 61 YLQKPGQSPOLLITGYSNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 DB 61 YLQKPGQSPOLLITGYSNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 119
 OY 121 YTFGGGTKEIKRADAAP 138
 DB 121 YTFGGGTKEIKRADAAP 137

RESULT 12

W14937
 ID W14937 standard; Protein: 238 AA.

AC W14937:
 DT 16-JUN-1997 (first entry)
 DE Murine anti-porcine VCAM 3F4 light chain.
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KM Vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KM chimeric antibody; diagnosis.
 OS Mus sp.
 FH Key
 FT region Location/Qualifiers
 FT /label= CDR1
 FT /label= CDR2
 FT /label= CDR3
 FT region
 FT region
 PN MO9711971-A1.
 PD 03-APR-1997.
 PF 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matlis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR N-PSDB: T62934.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure: Page 52-53; 105pp; English.
 CC Light chain (W14937) and heavy chain (W14938) sequences are
 CC provided for the murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody (MAb) 3F4. Hybridoma 3F4 was
 CC produced by standard techniques using recombinant, soluble porcine
 CC VCAM as immunogen. Chimeric antibodies can be produced by cloning
 CC MAb 3F4 and 2A2 (see also W14931-32) variable regions into
 CC expression plasmid pAPEX-3P modified to contain the human gamma4
 CC constant region in place of the human gamma1 C1 region. Sequences
 CC are provided for 3F4 (chimeric) human G2/G4 cDNA (W14939), a 3F4
 CC human G2/G4 expression plasmid insert product (W14940), and 3F4
 CC human IgG4 expression plasmid insert products (W14941-42). The
 CC chimeric antibodies are specific for porcine VCAM. They are useful
 CC for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs
 CC into human recipients.
 SQ Sequence 238 AA;

Query Match 79.8%; Score 574.5; DB 1; Length 238;
 Best Local Similarity 81.2%; Pred. No. 2.1e-35;
 Matches 11; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

OY 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEPASISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEPASISCRSSQSLAKSYGNTYLSW 59
 OY 61 YLQKPGQSPOLLITGYSNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 DB 61 YLQKPGQSPOLLITGYSNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 119

QY 121 YTFGGGKVEIKRADAP 138
 DB 120 FTFGGGKLEIKRTVAAP 137

RESULT 13

W34518
 ID W34518 standard; Protein; 131 AA.
 AC W34518;
 DT 19-MAR-1998 (first entry)
 DE Variable kappa chain of antibody from hybridoma 1-706-139.
 KW Variable region coding sequence; constant region epitope; hybridoma;
 KW antibody detection; antigen/antibody complex; variable heavy chain.
 OS Mus musculus.
 PN WO9727486-A1.
 PD 31-JUL-1997.
 PF 17-JAN-1997; 001074.
 PR 23-JAN-1996; US-589939.
 PA (ABBO) ABBOTT LAB.
 PI Golden AM, Hackett JR, Hoff JA, Ostrow DH;
 DR WPI: 97-393833/36.
 DR N-PSDB: T98835.
 PT Use of antibody constant region epitope(s) - as control or
 PT calibrator reagents in assays for detecting the presence of an
 PT antibody in a test sample
 PS Disclosure; Page 62-63; 109pp; English.
 CC This sequence represents the variable kappa chain of the antibody
 CC produced by hybridoma 1-706-139, and can be detected using the method of
 CC the invention. The method is for detecting the presence of antibody which
 CC may be present in a test sample. It comprises contacting a test sample
 CC suspected of containing the antibody with an antigen specific for the
 CC antibody to allow the formation of antigen/antibody complexes, detecting
 CC the presence of the antibody which may be present in the test sample and
 CC employing, as a control or calibrator a reagent which binds to the
 CC antigen. The improvement to this method over previous methods, comprises
 CC employing, as the control or calibrator, a reagent comprising one or more
 CC antibody constant region epitopes, where the reagent binds to the antigen
 CC and is homogeneous with respect to specificity and affinity. The method
 CC can be also be used for detecting the presence of antibodies developed
 CC against more than one antigen. The method is used particularly for the
 CC detection of human antibodies specific for a given antigen, e.g. HIV-1,
 CC hepatitis E virus, rubella virus, etc. Use of the reagents circumvent all
 CC of the problems associated with using an immune sera in the manufacture
 CC of calibrators and positive controls. The present reagents can be readily
 CC and reproducibly generated in virtually unlimited quantities and are also
 CC useful for quantitating, and monitoring the integrity of, the antigen
 CC used in assays.
 SQ Sequence 131 AA;

Query Match 79.2%; Score 570.5; DB 1; Length 131;

Best Local Similarity 82.6%; Pred. No. 2.3e-35; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPSGDVVMTQSPSLPYTPGPASISCRSSOSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPSGDVVMTQSPSLPYTPGPASISCRSSOSLAKSYGNTYLSW 59
 QY 61 YLQKPGSPQLLYIGISNRSFGVDPDRFSGSGSTDFTLKISRVAEDVGYTCLOGTHOP 120
 DB 60 YLQKPGSPQLLYIKVSNRSGVDPDRFSGSGSTDFTLKISRVAEDLGYFCQSQSTHPV 119
 QY 121 YTFGGGKVEIK 132
 DB 120 WTFGGGKLEIK 131

RESULT 14

W31752
 ID W31752 standard; Protein; 238 AA.
 AC W31752;
 DT 15-APR-1998 (first entry)

DE L chain subunit of Fas specific antibody.
 KW Fas; antibody; human; immunoglobulin; variable region; rheumatism;
 KW autoimmune disease; rheumatoid arthritis; therapy; CDR; heavy chain;
 KW complementarity determining region.
 OS Mus musculus.

FN Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note= "signal peptide"
 FT /note= "mature protein"

PN EP-799891-A1.
 PD 08-OCT-1997.
 PF 27-MAR-1997; 302415.
 PR 01-APR-1996; JP-078570.
 PA (SANY) SANKYO CO LTD.
 PI Ichikawa K, Nakahara K, Serizawa N, Yonehara S;
 DR WPI: 97-482673/45.
 DR N-PSDB: T88870.
 PT Anti-Fas recombinant antibodies - useful for treating auto-immune
 PT diseases, especially rheumatoid arthritis
 PS Claim 12; Page 34-35; 72pp; English.
 CC This sequence represents the light chain of the protein of the invention.
 CC The protein of the invention is a recombinant protein (A), that comprises
 CC at least one region corresponding to an immunoglobulin (Ig) variable
 CC region which enables the protein to recognise and specifically bind to an
 CC antigen, preferably human Fas, and has substantially no more
 CC immunogenicity in a human patient than a human antibody. The proteins are
 CC useful for treating autoimmune diseases, especially rheumatism
 CC (rheumatoid arthritis). (A) is based on a murine monoclonal antibody. As
 CC the protein lacks the constant region, it has substantially no more
 CC immunogenicity in the human patient than a human antibody.
 SQ Sequence 238 AA;

Query Match 79.2%; Score 570.5; DB 1; Length 238;

Best Local Similarity 81.2%; Pred. No. 4.1e-35; Mismatches 16; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPSGDVVMTQSPSLPYTPGPASISCRSSOSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPSGDVVMTQSPSLPYTPGPASISCRSSOSLAKSYGNTYLSW 59
 QY 61 YLQKPGSPQLLYIGISNRSFGVDPDRFSGSGSTDFTLKISRVAEDVGYTCLOGTHOP 120
 DB 60 YLQKPGSPQLLYIKVSNRSGVDPDRFSGSGSTDFTLKISRVAEDLGYFCQSQSTHPV 119
 QY 121 YTFGGGKVEIKRADAP 138
 DB 120 PAFGGGKLEIKRADAP 137

RESULT 15

W71889
 ID W71889 standard; Protein; 238 AA.
 AC W71889;
 DT 18-JAN-1999 (first entry)
 DE Anti-human Fas monoclonal antibody CH11 light chain.
 KW Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human; mouse;
 KW antibody engineering.
 OS Synthetic.
 OS Mus musculus.

FN Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= sig_peptide
 FT /label= Mat_protein
 FT Region 43..58
 FT /label= CDR1
 FT Region 74..80
 FT /label= CDR2
 FT Region 113..121
 FT /label= CDR3

PN EP-866131-A2;
 PD 23-SEP-1998.
 PF 20-MAR-1998; 302113.
 PR 21-MAR-1997; JP-067938.
 PA (SANKYO) SANKYO CO LTD.
 PI Hanyama H, Nakahara K, Serizawa N, Takahashi T,
 PI Yonehara S;
 DR WPI; 98-482965/42.
 DR N-PSDB; V66736.
 PT Production of anti-Fas protein humanised antibodies - for use in
 PT inducing apoptosis on Fas expressing cells in the treatment of
 PT autoimmune diseases, especially rheumatoid arthritis
 PS Reference Example 4; Page 62-63; 187pp; English.
 CC This is the amino acid sequence of the light chain of the
 CC mouse anti-human Fas monoclonal antibody CH1, as deduced from an
 CC amplified cDNA clone (see V66736). The invention relates to novel
 CC humanised antibodies comprising humanised light and heavy chains
 CC (see W71876-81) of CH1. These humanised anti-human Fas antibodies
 CC are capable of inducing apoptosis in cells expressing Fas (e.g.
 CC synovialocytes) and are useful in the treatment of autoimmune disease
 CC and chronic rheumatoid arthritis.
 SQ Sequence 238 AA;

Query Match 79.2%; Score 570.5; DB 1; Length 238;
 Best Local Similarity 81.2%; Pred. No. 4.1e-35;
 Matches 112; Conservative 9; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLLFPIVPSGDDVMTOSPLPYTPGPAPASISCRSSOSLAKSYGNTYLSW 60
 Db 1 MKLPVRLV-LMFPIVPSGDDVMTOSPLPYTPGPAPASISCRSSOSLAKSYGNTYLSW 59
 QY 61 YLQKPGQSPQLLYIGISNRPESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCLOGTHP 120
 Db 60 YLQKPGQSPKLLIKYVSNRPESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSGSTHP 119
 QY 121 YTFGGGTGVKIRADAAP 138
 Db 120 PAFGGGTGLEIKRADAAP 137

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